

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:25:38 ; Search time 130 Seconds
(without alignments)
94.635 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQIDALEYENDALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 9880

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	28	AAB74343	Aab74343 Peptide S
2	132	100.0	28	AAB74351	Aab74351 Peptide S
3	132	100.0	28	ADM41436	Adm41436 Self-asse
4	129	97.7	28	AAB74341	Aab74341 Peptide S
5	129	97.7	28	AAB74342	Aab74342 Peptide S
6	85	64.4	28	ADM41438	Adm41438 Self-asse
7	82	62.1	28	AAB74345	Aab74345 Peptide S
8	76	57.6	28	AAB74348	Aab74348 Peptide S
9	76	57.6	28	AAB74356	Aab74356 Peptide u
10	76	57.6	28	AAB74352	Aab74352 Peptide S
11	75	56.8	28	AAB74346	Aab74346 Peptide S
12	75	56.8	28	AAB74347	Aab74347 Peptide S
13	74	56.1	28	AAB74349	Aab74349 Peptide S
14	70	53.0	28	AAB74355	Aab74355 Peptide u
15	70	53.0	28	AAB74350	Aab74350 Peptide S
16	57	43.2	28	ABR84737	ABr84737 DE novo d
17	54	40.9	28	ABR84736	ABr84736 DE novo d
18	51	38.6	28	ABR84739	ABr84739 Integrin
19	51	38.6	28	ABR59138	ABr59138 Alpha-bel
20	46	34.8	28	AAK31979	Aak31979 SSP4 poly
21	45	34.1	28	ABR84735	ABr84735 DE novo d
22	41	31.1	28	ADT02245	Adt02245 Surface p
23	40	30.3	28	AAK31981	Aak31981 SSP7 poly
24	40	30.3	28	AAK78256	Aak78256 SSP(7)4 h

25	40	30.3	28	6	ADA15966	Ada15966 Synthetic
26	40	30.3	28	6	ABO44343	AbO44343 Ear I-bas
27	40	30.3	28	9	ADM71693	Adm71693 Peptide S
28	38	28.8	28	2	AAR76756	Aar76756 E. coli F
29	37	28.0	28	2	AAR32693	Aar32693 SSP poly
30	37	28.0	28	2	AAR32689	Aar32689 SSP poly
31	37	28.0	28	2	AAK31980	Aak31980 SSP(5)4 h
32	37	28.0	28	2	AAK78255	Aak78255 SSP 5.5.5
33	37	28.0	28	2	AAK78250	Aak78250 SSP 5.5.5
34	37	28.0	28	2	AAK78244	Aak78244 SSP 5.5.5
35	37	28.0	28	2	AAK78242	Aak78242 SSP 5.5.5
36	37	28.0	28	2	AAW62935	Aaw62935 Minimalis
37	37	28.0	28	2	AAW62947	Aaw62947 Minimalis
38	37	28.0	28	2	AAW60508	Aaw60508 Synthetic
39	37	28.0	28	2	AAW60516	Aaw60516 Synthetic
40	37	28.0	28	2	AAW60510	Aaw60510 Synthetic
41	37	28.0	28	2	AAW87744	Aaw87744 Synthetic
42	37	28.0	28	2	AAW87746	Aaw87746 Synthetic
43	37	28.0	28	2	AAW87748	Aaw87748 Synthetic
44	37	28.0	28	4	AAE11041	Aae11041 Leucine z
45	37	28.0	28	4	AAE11042	Aae11042 Leucine z

ALIGNMENTS

RESULT 1
AAB74343
ID AAB74343 standard; peptide; 28 AA.
XX AAB74343;
AC
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-plC.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
FN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX Claim 16; Page 26; 45pp; English.
PS The present invention relates to a protein structure with several first
XX peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-plC
XX Sequence 28 AA;
SQ

Query Match 100.0%; Score 132; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIAALKQKIASLKQIDALEYENDALEQ 28

PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Claim 16; Page 26; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-p1A
 XX Sequence 28 AA;
 SQ

Query Match 97.7%; Score 129; DB 4; Length 28;
 Best Local Similarity 96.4%; Pred. No. 8e-11; Indels 0; Gaps 0;
 Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQIEDALEYENDALEQ 28
 Db 1 KIAALKQKIASLKQIEDALEYENDALEQ 28

RESULT 5
 AAB74342
 ID AAB74342 standard; peptide; 28 AA.
 XX AAB74342;
 AC AAB74342;
 DT 02-JUL-2001 (first entry)
 XX Peptide SAF-p1B.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB003576.
 XX 17-SEP-1999; 99GB-00022013.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Disclosure; Page 9; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-p1B
 XX Sequence 28 AA;
 SQ

Query Match 97.7%; Score 129; DB 4; Length 28;
 Best Local Similarity 96.4%; Pred. No. 8e-11; Indels 0; Gaps 0;
 Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQIEDALEYENDALEQ 28
 Db 1 KIAALKQKIASLKQIEDALEYENDALEQ 28

RESULT 6
 AAB74345
 ID AAB74345 standard; peptide; 28 AA.
 XX AAB74345;
 AC AAB74345;
 DT 02-JUL-2001 (first entry)
 XX Peptide SAF-p2A.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.

ADM41438
 ID ADM41438 standard; peptide; 28 AA.
 XX ADM41438;
 AC ADM41438;
 DT 03-JUN-2004 (first entry)
 XX Self-assembling peptide fibre SAF-p2a.
 DE Fibre-shaping peptide; self-assembling peptide.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal NH3 moiety"
 FT WO2004022584-A1.
 XX 18-MAR-2004.
 XX 08-SEP-2003; 2003WO-GB003900.
 XX 06-SEP-2002; 2002GB-00020805.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson D, Ryadnov MG;
 XX WPI; 2004-248444/23.
 XX Novel fiber-shaping peptide comprising hub and several peptide monomer
 PT units, useful for producing protein structure useful in purification of
 PT biological fluids and in surface engineering procedures.
 XX Example 36; Page 22; 37pp; English.
 XX The present sequence is that of self-assembling peptide fibre (SAF) SAF-
 CC p2a. The invention relates to fibre-shaping (Fish) peptides ADM41434-
 CC ADM41435 that are capable of interacting with SAFs to form protein
 CC structures. The Fish peptides allow morphological changes (branches,
 CC splits, kinks and bends) to be made to protein fibres comprising SAFs. By
 CC incorporating such morphological changes in the protein structures, it is
 CC possible to generate a variety of (nanoscale) protein structures, such as
 CC assemblies in general, including matrix, filter, network, grid and
 CC scaffold structures. Use of the protein structures in the purification of
 CC biological fluids, for assembling cells for cell and tissue engineering,
 CC and in surface engineering procedures is claimed.
 XX Sequence 28 AA;
 SQ

Query Match 64.4%; Score 85; DB 8; Length 28;
 Best Local Similarity 75.0%; Pred. No. 0.00011; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQIEDALEYENDALEQ 28
 Db 1 KIRRLKQKIASLKQIEDALEYENDALEQ 28

RESULT 7
 AAB74345
 ID AAB74345 standard; peptide; 28 AA.
 XX AAB74345;
 AC AAB74345;
 DT 02-JUL-2001 (first entry)
 XX Peptide SAF-p2A.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.

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XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX PFPI; 2001-335468/35.
XX PT New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2A
XX SQ Sequence 28 AA;

Query Match 62.1%; Score 82; DB 4; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.00029;
Matches 21; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQEIADALEYENDALEQ 28
   ||||| ||||| ||||| |||||
Db 1 KISALKKKNASLKQEIADALEYENDALEQ 28

RESULT 8
AAB74348
ID AAB74348 standard; peptide; 28 AA.
XX AC AAB74348;
XX DT 02-JUL-2001 (first entry)
XX DE Peptide SAF-p2D.
XX KW Atomic Force Microscopy; AFM.
XX OS Unidentified.
XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX PFPI; 2001-335468/35.
XX PT New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2D
XX SQ Sequence 28 AA;

Query Match 57.6%; Score 76; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.002;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQEIADALEYENDALEQ 28
   ||||| ||||| ||||| |||||
Db 1 KIRALKAKNAHLKQEIADALEYENDALEQ 28

RESULT 9
AAB74356
ID AAB74356 standard; peptide; 28 AA.
XX AC AAB74356;
XX DT 02-JUL-2001 (first entry)
XX DE Peptide used to form blunt-ended heterodimers.
XX KW Atomic Force Microscopy; AFM.
XX OS Unidentified.
XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX PFPI; 2001-335468/35.
XX PT New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Fig 8; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is a peptide used to form blunt-ended heterodimers.
XX SQ Sequence 28 AA;

Query Match 57.6%; Score 76; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.002;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQEIADALEYENDALEQ 28
   ||||| ||||| ||||| |||||
Db 1 KIRALKAKNAHLKQEIADALEYENDALEQ 28

RESULT 10
AAB74352
ID AAB74352 standard; peptide; 28 AA.
XX AC AAB74352;
XX PFPI; 2001-335468/35.
XX PT New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first

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DT 02-JUL-2001 (first entry)
 XX Peptide SAP-p2.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB003576.
 XX 17-SEP-1999; 99GB-00022013.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Claim 16; Page 26; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAP-p2
 XX Sequence 28 AA;
 SQ Query Match 57.6%; Score 76; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.002; 8; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 OY 1 KIAALKQKIASLKQEIADALEYENDALEQ 28
 DB 1 KIRALKKWNHLKQEIADALEYENDALEQ 28
 RESULT 11
 AAB74346
 ID AAB74346 standard; peptide; 28 AA.
 AC AAB74346;
 XX 02-JUL-2001 (first entry)
 DT Peptide SAP-p2B.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB003576.
 XX 17-SEP-1999; 99GB-00022013.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Claim 16; Page 26; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAP-p2
 XX Sequence 28 AA;
 SQ Query Match 56.8%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0027; 8; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 OY 1 KIAALKQKIASLKQEIADALEYENDALEQ 28
 DB 1 KIRALKKWNHLKQEIADALEYENDALEQ 28
 RESULT 12
 AAB74347
 ID AAB74347 standard; peptide; 28 AA.
 AC AAB74347;
 XX 02-JUL-2001 (first entry)
 DT Peptide SAF-p2C.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB003576.
 XX 17-SEP-1999; 99GB-00022013.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Claim 16; Page 26; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-p2C
 XX Sequence 28 AA;
 SQ Query Match 56.8%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0027; 8; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 OY 1 KIAALKQKIASLKQEIADALEYENDALEQ 28
 DB 1 KIRALKKWNHLKQEIADALEYENDALEQ 28

```
RESULT 13
AAB74349
ID AAB74349 standard; peptide; 28 AA.
XX
XX AAB74349;
AC
XX
XX 02-JUL-2001 (first entry)
XX
XX Peptide SAF-p2E.
DE
XX Atomic Force Microscopy; AFM.
XX
XX Unidentified.
OS
XX
XX WO200121646-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 18-SEP-2000; 2000WO-GB003576.
PF
XX
XX 17-SEP-1999; 99GB-00022013.
PR
XX
XX (UYSU-) UNIV SUSSEX.
PA
XX
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
PI
XX WPI; 2001-335468/35.
DR
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 9; 45pp; English.
PS
XX
XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p2E
XX
XX Sequence 28 AA;
SQ
Query Match 56.1%; Score 74; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0037;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIRALKKIKIASLKQETDALEYENDALEQ 28
DB 1 KIRALKCKNAHLKQETAALESQETAALEQ 28

RESULT 14
AAB74355
ID AAB74355 standard; peptide; 28 AA.
XX
XX AAB74355;
AC
XX
XX 02-JUL-2001 (first entry)
XX
XX Peptide used to form blunt-ended heterodimers.
DE
XX Atomic Force Microscopy; AFM.
XX
XX Unidentified.
OS
XX
XX WO200121646-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 18-SEP-2000; 2000WO-GB003576.
PF
XX
XX 17-SEP-1999; 99GB-00022013.
PR
XX
XX (UYSU-) UNIV SUSSEX.
PA
XX
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
PI
XX WPI; 2001-335468/35.
DR
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 12; 45pp; English.
PS
XX
XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p3
XX
XX Sequence 28 AA;
SQ
Query Match 53.0%; Score 70; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIDALEYENDALEQ 28
DB 1 EIDALEYENDALEQ 14

RESULT 15
AAB74350
ID AAB74350 standard; peptide; 28 AA.
XX
XX AAB74350;
AC
XX
XX 02-JUL-2001 (first entry)
XX
XX Peptide SAF-p3.
DE
XX Atomic Force Microscopy; AFM.
XX
XX Unidentified.
OS
XX
XX WO200121646-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 18-SEP-2000; 2000WO-GB003576.
PF
XX
XX 17-SEP-1999; 99GB-00022013.
PR
XX
XX (UYSU-) UNIV SUSSEX.
PA
XX
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
PI
XX WPI; 2001-335468/35.
DR
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 12; 45pp; English.
PS
XX
XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p3
XX
XX Sequence 28 AA;
SQ
Query Match 53.0%; Score 70; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIDALEYENDALEQ 28
DB 1 EIDALEYENDALEQ 14

RESULT 16
ABR84737
ID ABR84737 standard; peptide; 28 AA.
XX
AC ABR84737;
XX
DT 18-DEC-2003 (first entry)
XX
DE DE novo designed AHEC peptide #5.
XX
KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KW AHEC; antiparallel; drug targeting.
XX
OS Synthetic.
XX
PN WO2003066660-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001217.
XX
PR 05-FEB-2002; 2002US-0354376P.
XX
PA (IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX
PI Caterer NR, Uttental LO, Neilson RW;
XX
PS WPI; 2003-679535/64.
XX
CC Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX
PS Disclosure; Page 14; 35pp; English.
XX
CC The present invention relates to a composition which comprises a pair of antibody Fv fragments linked and stabilised by antiparallel heterogeneous alpha-helical coiled-coil (AHEC) peptides. The composition is used to form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the targeting of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
XX
SQ Sequence 28 AA;

Query Match 40.9%; Score 54; DB 7; Length 28;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDAILE 20
DB 5 KIAAIEKIAQIBETAAQE 24

RESULT 18
AAB50879
ID AAB50879 standard; peptide; 28 AA.
XX
AC AAB50879;
XX
DT 19-MAR-2001 (first entry)
XX
DE Integrin cytoplasmic domain heptad-repeat.
XX
KW Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
KW multiple sclerosis; asthma; atherosclerosis; wound healing;
KW cytoplasmic domain; heptad-repeat.
XX
OS Homo sapiens.
XX
PN WO200073342-A1.
XX
PD 07-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US015153.
XX
PR 01-JUN-1999; 99US-00323447.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ginsberg MH, Pfaff M, Liu S;

Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIDALEYENDALEQ 28
DB 1 EIDALEYENDALEQ 14

RESULT 16
ABR84737
ID ABR84737 standard; peptide; 28 AA.
XX
AC ABR84737;
XX
DT 18-DEC-2003 (first entry)
XX
DE DE novo designed AHEC peptide #5.
XX
KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KW AHEC; antiparallel; drug targeting.
XX
OS Synthetic.
XX
PN WO2003066660-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001217.
XX
PR 05-FEB-2002; 2002US-0354376P.
XX
PA (IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX
PI Caterer NR, Uttental LO, Neilson RW;
XX
PS WPI; 2003-679535/64.
XX
CC Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX
PS Disclosure; Page 14; 35pp; English.
XX
CC The present invention relates to a composition which comprises a pair of antibody Fv fragments linked and stabilised by antiparallel heterogeneous alpha-helical coiled-coil (AHEC) peptides. The composition is used to form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the targeting of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
XX
SQ Sequence 28 AA;

Query Match 43.2%; Score 57; DB 7; Length 28;
Best Local Similarity 60.0%; Pred. No. 0.88; Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDAILE 20
DB 5 KQAIKNEIAIKQEIATIE 24

RESULT 17
ABR84736
ID ABR84736 standard; peptide; 28 AA.
XX
AC ABR84736;
XX
DT 18-DEC-2003 (first entry)
XX
DE DE novo designed AHEC peptide #4.

KW	infectious disease; food poisoning; Alzheimer's disease;
KW	amyloid beta-peptide; dental; MHC; major histocompatibility complex.
XX	Unidentified.
XX	WO2004087767-A1.
XX	14-OCT-2004.
XX	29-MAR-2004; 2004WO-JP004460.
XX	31-MAR-2003; 2003JP-00093243.
XX	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX	Nishizawa T;
XX	WPI; 2004-737672/72.
XX	New polypeptide having a sequence in which an adhesion motif of a cell
XX	adhesion molecule is bonded to a polypeptide comprising a T cell epitope
XX	and a B cell epitope, and a linker peptide, useful for producing
XX	antibodies.
XX	Example 6; SEQ ID NO 22; 71pp; Japanese.
XX	The invention relates to a novel polypeptide capable of inducing the
XX	potentiation of antibody production when transmemorally having a sequence
XX	in which the amino acid sequence of an adhesion motif of a cell adhesion
XX	molecule is bonded to the polypeptide. The novel polypeptide comprises a
XX	peptide consisting of an amino acid sequence of a T cell epitope's amino
XX	terminal side and the amino acid sequence of a B cell epitope's carboxy
XX	terminal side and having a linker peptide between the amino acid
XX	sequences. The invention further comprises: novel DNA or RNA which
XX	encodes the polypeptide; microorganisms or animals and plants which have
XX	the DNA or RNA introduced; and a composition comprising the novel
XX	polypeptide and an additive for the formulation. The novel polypeptide
XX	has the following activities: antibacterial, neuroprotective, nootropic,
XX	and virucide. The novel polypeptide, encoding polynucleotide or
XX	composition are useful for producing antibodies in animals, for
XX	preventing or treating diseases. The novel polypeptide is useful as an
XX	adjuvant to increase the antibody production against antigenic proteins.
XX	The novel polypeptide is useful for producing an antibody against toxins
XX	of a pathogenic virus and microorganisms, thus effective in preventing or
XX	treating infectious disease such as food poisoning. The novel polypeptide
XX	is useful for treating Alzheimer's disease by producing an antibody
XX	against amyloid beta-peptide. The novel polypeptide is also useful for
XX	treating dental caries. This sequence represents a peptide relating to
XX	the antibody production of the invention.
XX	Sequence 28 AA;
XX	Query Match 31.1%; Score 41; DB 8; Length 28;
XX	Best Local Similarity 50.0%; Pred. No. 1.5e+02;
XX	Matches 12; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY	3 AALKOKIASLKOETDAL--EYEND 24
DB	4 AALKQYEDALKKTYEALKQYED 27
XX	RESULT 23
XX	AAR31981
XX	ID AAR31981 standard; peptide; 28 AA.
XX	AC AAR31981;
XX	25-MAR-2003 (revised)
XX	22-JUN-1993 (first entry)
XX	SSP7 polypeptide, suitable for in vivo expression.
XX	Heptad; plants; custom tailored storage proteins.

KW	1 KIAALKOKIASLKOETDALE 20
DB	4 KIKALEKLEKALEKLEKALE 23
XX	RESULT 21
XX	ABR84735
XX	ID ABR84735 standard; peptide; 28 AA.
XX	AC ABR84735;
XX	18-DEC-2003 (first entry)
XX	DE novo designed AHEC peptide #3.
XX	Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
XX	AHEC; antiparallel; drug targeting.
XX	Synthetic.
XX	WO2003066660-A2.
XX	14-AUG-2003.
XX	05-FEB-2003; 2003WO-EP001217.
XX	05-FEB-2002; 2002US-0354376P.
XX	(IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX	Caterer NR, Uttental LO, Neilson RW;
XX	WPI; 2003-679535/64.
XX	Composition useful for forming therapeutic antibodies and antibody
XX	fragments comprises pair of antibody Fv fragments linked and stabilized
XX	by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX	Disclosure; Page 14; 35pp; English.
XX	The present invention relates to a composition which comprises a pair of
XX	antibody Fv fragments linked and stabilised by antiparallel heterogeneous
XX	alpha-helical coiled-coil (AHEC) peptides. The composition is used to
XX	form multimeric complexes and therapeutic antibodies and antibody
XX	fragments useful for e.g. inhibition of receptor binding and the
XX	targeting of drugs, toxins and labels in research, industry and
XX	healthcare. The present sequence is an AHEC peptide used in the
XX	exemplification of the invention
XX	Sequence 28 AA;
XX	Query Match 34.1%; Score 45; DB 7; Length 28;
XX	Best Local Similarity 56.2%; Pred. NO. 41;
XX	Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY	1 KIAALKOKIASLKOET 16
DB	12 EIAAKDKIAAKIKEYI 27
XX	RESULT 22
XX	ADT02245
XX	ID ADT02245 standard; peptide; 28 AA.
XX	AC ADT02245;
XX	30-DEC-2004 (first entry)
XX	Surface protein antigen (Pac) peptide, SEQ ID 22.
XX	potentiation; antibody production; cell adhesion; T cell; B cell;
XX	epitope; antibacterial; neuroprotective; nootropic; virucide;

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XX OS Synthetic.
XX PN WO9303160-A1.
XX PD 18-FEB-1993.
XX PF 07-AUG-1992; 92WO-US006412.
XX PR 09-AUG-1991; 91US-00743006.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Falco SC, Keeler SJ, Rice JA;
XX DR WPI; 1993-076517/09.
XX PT Synthetic polypeptide(s) contg. specified heptad units - expressed in
XX PT vivo in plants to serve as custom-tailored storage proteins with
XX PT specified aminoacid content.
XX PS Claim 7; Page 103; 176pp; English.
XX CC The sequence represents a synthetic polypeptide comprising heptad units
XX CC of the peptide. The synthetic polypeptide can be expressed in vivo in
XX CC plants to serve as a synthetic seed storage protein which can be custom-
XX CC tailored for specific end-user requirements. The DNA encoding the heptad
XX CC may be used to transform plants to increase the content of partic. amino
XX CC acids such as lysine or methionine in seeds or leaves. See also AAR31979-
XX CC 86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 28 AA;

Query Match 30.3%; Score 40; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

OY 1 KIAALKOKIASLKQEIADALE 20
Db 4 KLRAMEEKLKAMEEKLKAME 23

RESULT 24
ADA15966
ID AAR78256 standard; peptide; 28 AA.
XX AC AAR78256;
XX DT 15-JUL-1996 (first entry)
XX DE SSP(7)4 heptad.
XX LYsine; synthetic storage protein; SSP; vector; PSK6;
XX dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
XX Glycine max; transgenic plant; essential amino acid.
XX OS Synthetic.
XX PN WO9515392-A1.
XX PD 08-JUN-1995.
XX PF 21-NOV-1994; 94WO-US013190.
XX PR 30-NOV-1993; 93US-00160117.
XX PR 17-JUN-1994; 94US-00261661.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Falco SC, Keeler SJ, Rice JA;
XX DR WPI; 1995-215272/28.
XX DR N-PSDB; AAQ95000.

Query Match 30.3%; Score 40; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

OY 1 KIAALKOKIASLKQEIADALE 20
Db 4 KLRAMEEKLKAMEEKLKAME 23

RESULT 25
ADA15966
ID ADA15966 standard; peptide; 28 AA.
XX AC ADA15966;
XX DT 06-NOV-2003 (first entry)
XX DE Synthetic storage protein, SSP, peptide SSP(7)4.
XX LYsC; transgenic; lysine accumulation; dihydrodipicolinic acid synthase;
XX DHDPs; lysine inhibition; lysine ketoglutarate reductase; LKR;
XX chloroplast transit sequence; CTS; aspartokinase III; AKIII;
XX synthetic seed storage protein; SSP.
XX OS Synthetic.
XX PN US6459019-B1.
XX PD 01-OCT-2002.
XX PF 24-MAR-1997; 97US-00823771.
XX PR 19-MAR-1992; 92US-00855414.
XX PR 06-JAN-1994; 94US-00178212.
XX PR 07-JUN-1995; 95US-00474633.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Falco SC, Keeler SJ, Rice JA;
XX DR WPI; 2003-028272/02.
XX DR N-PSDB; ADA15964.
XX PT Transformed plants that accumulate lysine at higher levels in its seeds
XX PT than untransformed plants, has gene fragments encoding lysine-insensitive
XX PT dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
XX PS Example 21; Col 81; 109pp; English.
XX CC The invention relates to a plant comprising two foreign nucleotide
XX CC sequences which cause seeds obtained from the plant to accumulate lysine
XX CC at a level of at least 10% higher than seeds of a plant that do not
XX CC comprise the nucleotide, where the nucleotide comprises a fragment
XX CC encoding a dihydrodipicolinic acid synthase (DHDPs) that is insensitive
XX CC to lysine inhibition, and a fragment encoding a plant lysine

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XX PT New chimeric gene providing increased lysine content in plant seeds -
XX PT contains di:hydrodipicolinic acid synthase gene coupled to chloroplast
XX PT transport sequence and seed specific promoter, also new plants of
XX PT improved nutritional value.
XX PS Example 8; Page 81; 180pp; English.
XX CC Oligonucleotide SM98 (AAQ95000) and complementary sequence SM99
XX CC (AAQ95001) code for 4 repeats (AAR78256) of heptad peptide SSP7 (see also
XX CC AAR78237). Clone 5-1 (AAQ95005) was obtd. by insertion of the
XX CC oligonucleotides into the Earl site of clone 84-H3 (see AAQ94993) and
XX CC transformation of Escherichia coli DH5 alpha. Synthetic storage protein
XX CC SSPs-1 (AAR78259) encoded by the construct can be used to raise the
XX CC lysine content in seeds of transformed plants
XX SQ Sequence 28 AA;

Query Match 30.3%; Score 40; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

OY 1 KIAALKOKIASLKQEIADALE 20
Db 4 KLRAMEEKLKAMEEKLKAME 23

RESULT 25
ADA15966
ID ADA15966 standard; peptide; 28 AA.
XX AC ADA15966;
XX DT 06-NOV-2003 (first entry)
XX DE Synthetic storage protein, SSP, peptide SSP(7)4.
XX LYsC; transgenic; lysine accumulation; dihydrodipicolinic acid synthase;
XX DHDPs; lysine inhibition; lysine ketoglutarate reductase; LKR;
XX chloroplast transit sequence; CTS; aspartokinase III; AKIII;
XX synthetic seed storage protein; SSP.
XX OS Synthetic.
XX PN US6459019-B1.
XX PD 01-OCT-2002.
XX PF 24-MAR-1997; 97US-00823771.
XX PR 19-MAR-1992; 92US-00855414.
XX PR 06-JAN-1994; 94US-00178212.
XX PR 07-JUN-1995; 95US-00474633.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Falco SC, Keeler SJ, Rice JA;
XX DR WPI; 2003-028272/02.
XX DR N-PSDB; ADA15964.
XX PT Transformed plants that accumulate lysine at higher levels in its seeds
XX PT than untransformed plants, has gene fragments encoding lysine-insensitive
XX PT dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
XX PS Example 21; Col 81; 109pp; English.
XX CC The invention relates to a plant comprising two foreign nucleotide
XX CC sequences which cause seeds obtained from the plant to accumulate lysine
XX CC at a level of at least 10% higher than seeds of a plant that do not
XX CC comprise the nucleotide, where the nucleotide comprises a fragment
XX CC encoding a dihydrodipicolinic acid synthase (DHDPs) that is insensitive
XX CC to lysine inhibition, and a fragment encoding a plant lysine

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RESULT 30
AAR32689
ID AAR32689 standard; peptide; 28 AA.

XX AC AAR32689;
XX 25-MAR-2003 (revised)
XX 22-JUN-1993 (first entry)

XX SSF polypeptide produced from clone D16.

XX Heptad; plants; custom tailored storage proteins; in vivo; expression.
XX Synthetic.

XX WO9303160-A1.

XX 18-FEB-1993.

XX 07-AUG-1992; 92WO-US006412.

XX 09-AUG-1991; 91US-00743006.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Keeler SJ, Rice JA;

XX WPI; 1993-076517/09.

XX N-PSDB; AAQ3270.

XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
XX vivo in plants to serve as custom-tailored storage proteins with
XX specified aminoacid content.

XX Disclosure; Page 120; 176pp; English.

XX The sequence represents a synthetic heptad polypeptide which can be
XX expressed in vivo in plants to serve as a synthetic seed storage protein
XX which can be custom-tailored for specific end-user requirements. The DNA
XX encoding the heptad may be used to transform plants to increase the
XX content of partic. amino acids such as lysine or methionine in seeds or
XX leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-
XX MAR-2003 to correct PN field.)

XX Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKQSIDALE 20
|:|:|:|:|:|:|:|:|:|:
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 31

AAR31980
ID AAR31980 standard; peptide; 28 AA.

XX AC AAR31980;

XX 25-MAR-2003 (revised)

XX 22-JUN-1993 (first entry)

XX SSF5 polypeptide, suitable for in vivo expression.

XX Heptad; plants; custom tailored storage proteins.

XX Synthetic.

XX WO9303160-A1.

PN

XX 18-FEB-1993.
XX 07-AUG-1992; 92WO-US006412.
XX 09-AUG-1991; 91US-00743006.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Falco SC, Keeler SJ, Rice JA;
XX WPI; 1993-076517/09.

XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
XX vivo in plants to serve as custom-tailored storage proteins with
XX specified aminoacid content.

XX Claim 7; Page 102; 176pp; English.

XX The sequence represents a synthetic polypeptide comprising heptad units
XX of the peptide. The synthetic polypeptide can be expressed in vivo in
XX plants to serve as a synthetic seed storage protein which can be custom-
XX tailored for specific end-user requirements. The DNA encoding the heptad
XX may be used to transform plants to increase the content of partic. amino
XX acids such as lysine or methionine in seeds or leaves. See also AAR31979-
XX 86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKQSIDALE 20
|:|:|:|:|:|:|:|:|:|:
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 32

AAR78255
ID AAR78255 standard; peptide; 28 AA.

XX AC AAR78255;

XX 15-JUL-1996 (first entry)

XX SSP(S)4 heptad.

XX Lysine; synthetic storage protein; SSP; vector; pSK6;
XX dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
XX Glycine max; transgenic plant; essential amino acid.

XX Synthetic.

XX WO9515392-A1.

XX 08-JUN-1995.

XX 21-NOV-1994; 94WO-US013190.

XX 30-NOV-1993; 93US-00160117.

XX 17-JUN-1994; 94US-00261661.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Keeler SJ, Rice JA;

XX WPI; 1995-215272/28.

XX N-PSDB; AAQ94998.

XX New chimeric gene providing increased lysine content in plant seeds -
XX contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX transport sequence and seed specific promoter, also new plants of

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PT improved nutritional value.
XX
PS Example 8; Page 81; 180pp; English.
XX
CC Oligonucleotide SM96 (AAQ94998) and complementary sequence SM97
CC (AAQ94999) code for 4 repeats (AAR78255) of heptad peptide SSP5 (see also
CC (AAR78238). Clone 3-5 (AAQ95006) was obt'd. by insertion of the first 22
CC bases of the SM96-SM97 set into the EarI site of clone 82-4 (see
CC AAQ94992) and transformation of Escherichia coli DH5 alpha. Synthetic
CC storage protein SSP3-5 (AAR78260) encoded by the construct was used to
CC raise the lysine content in seeds of transformed tobacco, soybean and
CC corn
XX
SQ Sequence 28 AA;
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEI DALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 33
AAR78250
ID AAR78250 standard; protein; 28 AA.
XX
AC AAR78250;
XX
DT 15-JUL-1996 (first entry)
XX
DE SSP 5.5.5.5.
XX
KW Lysine; synthetic storage protein; SSP; vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
KW Glycine max; transgenic plant; essential amino acid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..7 /label= SSP5
FT Peptide 8..14 /label= SSP5
FT Peptide 15..21 /label= SSP5
FT Peptide 22..28 /label= SSP5
FT Peptide 22..28 /label= SSP5
XX
PN WO9515392-A1.
XX
PD 08-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US013190.
XX
PR 30-NOV-1993; 93US-00160117.
PR 17-JUN-1994; 94US-00261661.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1995-215272/28.
XX
DR N-PSDB; AAQ94993.
XX
PT New chimeric gene providing increased lysine content in plant seeds -
PT contains dihydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of
PT improved nutritional value.
XX
PS Example 8; Page 136; 180pp; English.
XX

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CC Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78250) comprises 2
CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
CC derived from vector pSK6. It was obt'd. by insertion of HPLC-purified SSP5
CC -encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the
CC resulting vector to transform Escherichia coli JM103, yielding clone 84-
CC H3 (AAQ94993). The SSP forms a coiled-coil structure. It can be expressed
CC in the seeds of transformed plants, e.g. soybean and corn, to increase
CC lysine content
XX
SQ Sequence 28 AA;
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEI DALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 34
AAR78244
ID AAR78244 standard; protein; 28 AA.
XX
AC AAR78244;
XX
DT 15-JUL-1996 (first entry)
XX
DE SSP 5.5.5.5.
XX
KW Lysine; synthetic storage protein; SSP; vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
KW Glycine max; transgenic plant; essential amino acid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..7 /label= SSP5
FT Peptide 8..14 /label= SSP5
FT Peptide 15..21 /label= SSP5
FT Peptide 22..28 /label= SSP5
FT Peptide 22..28 /label= SSP5
XX
PN WO9515392-A1.
XX
PD 08-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US013190.
XX
PR 30-NOV-1993; 93US-00160117.
PR 17-JUN-1994; 94US-00261661.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1995-215272/28.
XX
DR N-PSDB; AAQ94983.
XX
PT New chimeric gene providing increased lysine content in plant seeds -
PT contains dihydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of
PT improved nutritional value.
XX
PS Example 8; Page 129; 180pp; English.
XX
CC Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78244) comprises 2
CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
CC derived from vector pSK6. It was obt'd. by insertion of SSP5-encoding
CC oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector

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Query Match		28.0%; Score 37; DB 2; Length 28
Best Local Similarity		25.0%; Pred. No. 5.4e+02;
Matches	5; Conservative	12; Mismatches 3; Indels
QY	1 KIAALKKQKIASLKQEIDALE 20 : :: : : :: : :	
DB	4 KMKAMEEKMKAMEEKKMAE 23 : :: : : :: : :	
RESULT 36		
AAW62935		
ID	AAW62935 standard; peptide; 28 AA.	
XX		
AC	AAW62935;	
XX		
DT	02-OCT-1998 (first entry)	
XX		
DE	Minimalist lytic peptide.	
XX		
KW	Lytic peptide; channel forming peptide; antibacterial; am	
XX		
OS	Synthetic.	
XX	US5789542-A.	
PN		
XX	04-AUG-1998.	
DD		
PF	06-OCT-1997; 97US-00944133.	
XX		
PR	22-APR-1994; 94US-00232525.	
PR	22-JUL-1996; 96US-00681075.	
PR	03-FEB-1997; 97US-00789077.	
XX		
PA	(LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.	
XX		
PI	Becker CU, McLaughlin ML;	
XX		
DR	WPI; 1998-446183/38.	
XX		
PT	Selective lysis of bacteria amongst mammalian cells - usi	
PT	mer lytic peptides.	
XX		
PS	Disclosure; Col 5; 25pp; English.	
XX		
CC	AAW62920-67 represent minimalist lytic (channel forming)	
CC	peptides have antibacterial properties in concentrations	
CC	toward mammalian cells. The peptides are heptads (or hepta	
CC	that comprise four nonpolar amino acid residues and three	
CC	charged amino acid residues, or five nonpolar amino acid	
CC	positively charged amino acid residues. The nonpolar amin	
CC	and the positively charged amino acid residues are distrib	
CC	heptad such that when the multimer form an alpha-helix t	
CC	amino acid residues will lie on one face of the alpha-hel	
CC	positively charged amino acid residues will lie on the opo	
CC	the alpha -helix, whereby the multimer is amphipathic	
XX		
SQ	Sequence 28 AA;	
Query Match		28.0%; Score 37; DB 2; Length 28
Best Local Similarity		34.6%; Pred. No. 9.4e+02;
Matches	9; Conservative	8; Mismatches 9; Indels
Qy	2 IAALKKQKIASLKQEIDALEYENDALE 27 : : : : : : :	
Db	3 LKALKKALKKALKKALKKALKKALK 28 : : : : : : :	
RESULT 37		
AAW62947		
ID	AAW62947 standard; peptide; 28 AA.	
XX		
AC	AAW62947;	

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XX DT 02-OCT-1998 (first entry)
XX DE Minimalist lytic peptide.
XX KW Lytic peptide; channel forming peptide; antibacterial; amphipathic.
XX OS Synthetic.
XX PN US5789542-A.
XX PD 04-AUG-1998.
XX PF 06-OCT-1997; 97US-00944133.
XX PR 22-APR-1994; 94US-00232525.
XX PR 22-JUL-1996; 96US-00681075.
XX PR 03-FEB-1997; 97US-00789077.
XX (LOU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX PA Becker CL, McLaughlin ML;
XX PI WPI; 1998-446183/38.
XX DR Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-
XX mer lytic peptides.
XX PS Disclosure; Col 6; 25pp; English.
XX CC AAW6920-67 represent minimalist lytic (channel forming) peptides. The
XX peptides have antibacterial properties in concentrations not lethal
XX toward mammalian cells. The peptides are heptads (or heptad multimers)
XX that comprise four nonpolar amino acid residues and three positively
XX charged amino acid residues, or five nonpolar amino acid residues and two
XX positively charged amino acid residues. The nonpolar amino acid residues
XX and the positively charged amino acid residues are distributed within the
XX heptad such that when the multimer forms an alpha-helix the nonpolar
XX amino acid residues will lie on one face of the alpha-helix, and the
XX positively charged amino acid residues will lie on the opposite face of
XX the alpha-helix, whereby the multimer is amphipathic
XX SQ Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 36.0%; Pred. No. 5.4e+02;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 ALKQKTASLKQKIDALEYENDALEQ 28
   |||: : |||: : |||: |||:
Db 2 ALKALKALKALKALKALKALKK 26

RESULT 38
AAW60508
ID AAW60508 standard; protein; 28 AA.
XX
XX AC AAW60508;
XX DT 25-MAR-2003 (revised)
XX DT 25-AUG-1998 (first entry)
XX Synthetic storage protein of the specification.
XX KW Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein;
XX lysine inhibition; plant chloroplast transit sequence;
XX KW plant seed-specific regulatory sequence; transgenic plant;
XX KW increased lysine level; corn; Zea mays; soybean; Glycine max.
XX OS Synthetic.
XX PN US5773691-A.
XX

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQKIDALE 20
   |||: : |||: : |||: |||:
Db 4 KMKAMEEKMKAMEEKMAE 23

RESULT 39
AAW60516
ID AAW60516 standard; protein; 28 AA.
XX
XX AC AAW60516;
XX DT 25-MAR-2003 (revised)
XX DT 25-AUG-1998 (first entry)
XX Synthetic storage protein of the specification.
XX KW Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein;
XX lysine inhibition; plant chloroplast transit sequence;
XX KW plant seed-specific regulatory sequence; transgenic plant;
XX KW increased lysine level; corn; Zea mays; soybean; Glycine max.
XX OS Synthetic.
XX PN US5773691-A.
XX PD 30-JUN-1998.
XX PF 07-JUN-1995; 95US-00474633.
XX PR 19-MAR-1992; 92US-00855414.
XX PR 18-MAR-1993; 93WO-US002480.
XX PR 06-JAN-1994; 94US-00178212.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.

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XX Falco SC;
PI XX
XX WPI; 1998-387117/33.
DR N-PSDB; AAV35831.
XX
XX Chimeric genes encoding lysine production enzymes - useful for increasing
PT transgenic seed lysine content without being inhibited by high levels of
PT the amino acid.
XX
XX Example 21; Col 115-116; 106pp; English.
PS
XX The present sequence represents a synthetic lysine rich, storage protein
CC of the specification. The sequence can be operably linked to a seed-
CC specific regulatory sequence to create a chimeric gene of the
CC specification. The specification also describes a *Corynebacterium* dapA
CC gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme,
CC which was used to create chimeric genes of the invention. The chimeric
CC genes contain a nucleic acid fragment encoding a DHDPS enzyme which is
CC insensitive to inhibition by lysine operably linked to a plant
CC chloroplast transit sequence and to a plant seed-specific regulatory
CC sequence. The chimeric genes are useful for producing plants containing
CC increased levels of lysine, especially in corn (Zea mays) and soybean
CC (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 28 AA;
SQ

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0

Qy 1 KIAALKKQKIASLKQETDALE 20
|:|::|:|::|:|::|:|
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 41
AAW87744
ID AAW87744 standard; protein; 28 AA.
XX
XX AAW87744;
AC
XX
XX 29-MAR-1999 (first entry)
DT
XX
XX Synthetic lysine-rich storage protein 5.5.5.5.
DE
XX Lysine; transgenic plant; seed storage protein.
KW
XX Synthetic.
OS

Key Location/Qualifiers
FH Peptide 1..7
FT /label= SSP5
FT Peptide 8..14
FT /label= SSP5
FT Peptide 15..21
FT /label= SSP5
FT Peptide 22..28
FT /label= SSP5
XX
XX W09842831-A2.
XX
XX 01-OCT-1998.
XX
XX 27-MAR-1998; 98WO-US006051.
XX
XX 27-MAR-1997; 97US-00824627.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, Mcdevitt RE, Epelbaum SU;
PI WPI; 1999-045139/04.
XX N-PSDB; AAV99516.
DR
XX Nucleic acids and chimeric genes for increasing seed lysine content -
PT comprise sequence encoding all or part of lysine ketoglutarate reductase,
PT useful to improve nutritional quality of seeds from transformed plants.
XX
XX Example 21; Page 137; 231pp; English.
PS
XX This is the amino acid sequence of a lysine-rich synthetic seed storage
CC protein.

RESULT 45
AAE11042
ID AAE11042 standard; peptide; 28 AA.
XX AC AAE11042;
XX 18-DEC-2001 (first entry)
XX Leucine zipper peptide #4.
DE
XX Tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
KW melanoma; leucine zipper peptide.
XX
OS Unidentified.
XX US6284236-B1.
PN
XX 04-SEP-2001.
PD
XX 26-MAY-1999; 99US-00320424.
PF
XX 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
PR 25-JUN-1996; 96US-00670354.
PR 26-MAR-1998; 98US-00048641.
PR 10-NOV-1998; 98US-00190046.
XX
XX (IMMV) IMMUNEX CORP.
PA
XX Wiley SR, Goodwin RG;
PI
XX WPI; 2001-595463/67.
DR
XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
PT for treating viral infections (e.g. bovine viral diarrhea or human
PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX
XX Claim 11; Col 14; 4lpp; English.
XX
CC The invention relates to a cytokine designated as tumour necrosis factor
CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
CC of certain target cells, including cancer cells and virally infected
CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
CC treating viral infections (e.g. bovine viral diarrhoea or human
CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
CC melanoma), as a research reagent useful in studying apoptosis including
CC the regulation of programmed cell death. TRAIL DNA sequences may be
CC employed in developing a gene therapy approach to treating disorders
CC mediated by defective or insufficient amounts of TRAIL, in the production
CC of TRAIL polypeptides and as probes or primers in polymerase chain
CC reactions (PCR). The present sequence is a leucine zipper peptide that
CC promotes the trimerisation of TRAIL protein. The resulting trimeric TRAIL
CC protein has enhanced biological activity
XX
SQ Sequence 28 AA;
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 9 IASLKQEIADALE 20
|:::|:::|:::
Db 2 IASIRQQEIAIQ 13
Search completed: November 21, 2005, 21:40:23
Job time : 131 secs

Qy 1 KIAALKQKIASLKQEIADALE 20
|:|:::|:::|:::|:::
Db 4 KIKAMEEKMKAMEEKMKAME 23
RESULT 44
AAE11041
ID AAE11041 standard; peptide; 28 AA.
XX AC AAE11041;
XX 18-DEC-2001 (first entry)
XX Leucine zipper peptide #3.
DE
XX Tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
KW melanoma; leucine zipper peptide.
XX
OS Unidentified.
XX US6284236-B1.
PN
XX 04-SEP-2001.
PD
XX 26-MAY-1999; 99US-00320424.
PF
XX 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
PR 25-JUN-1996; 96US-00670354.
PR 26-MAR-1998; 98US-00048641.
PR 10-NOV-1998; 98US-00190046.
XX
XX (IMMV) IMMUNEX CORP.
PA
XX Wiley SR, Goodwin RG;
PI
XX WPI; 2001-595463/67.
DR
XX New tumor necrosis factor related apoptosis inducing ligand polypeptides
PT for treating viral infections (e.g. bovine viral diarrhea or human
PT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
XX
XX Claim 11; Col 14; 4lpp; English.
XX
CC The invention relates to a cytokine designated as tumour necrosis factor
CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
CC of certain target cells, including cancer cells and virally infected
CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
CC treating viral infections (e.g. bovine viral diarrhoea or human
CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
CC melanoma), as a research reagent useful in studying apoptosis including
CC the regulation of programmed cell death. TRAIL DNA sequences may be
CC employed in developing a gene therapy approach to treating disorders
CC mediated by defective or insufficient amounts of TRAIL, in the production
CC of TRAIL polypeptides and as probes or primers in polymerase chain
CC reactions (PCR). The present sequence is a leucine zipper peptide that
CC promotes the trimerisation of TRAIL protein. The resulting trimeric TRAIL
CC protein has enhanced biological activity
XX
SQ Sequence 28 AA;
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 9 IASLKQEIADALE 20
|:|:::|:::|:::|:::
Db 2 LASLRQLEALQ 13

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RESULT 3
A44877
cell surface protein 2F5 91K component - tobacco hornworm (fragment)
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44877
R;Nardi, J.B.
Dev. Biol. 152, 161-171, 1992
A;Title: Dynamic expression of a cell surface protein during rearrangement of epithelial
A;Reference number: A44877; MUID:92331807; PMID:1628754
A;Accession: A44877
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <NAR>
A;Cross-references: UNIPROT:Q9TWX0; UNIPARC:UPI000007FF81
A;Note: sequence extracted from NCBI backbone (NCBIP:108784)

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 8.6e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 12 LKQEIDALEVEN 23
DB 14 VKEQIESFEVIN 25

RESULT 4
S64701
hypothetical protein (aphl 5'-region) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S64701
R;Huang, Y.; Garrison, P.N.; Barnes, L.D.
Biochem. J. 312, 925-932, 1995
A;Title: Cloning of the Schizosaccharomyces pombe gene encoding diadenosine 5',5'-P(1)
n family.
A;Reference number: S64700; MUID:96128081; PMID:8554540
A;Accession: S64701
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <HUA>
A;Cross-references: UNIPARC:UPI000017B1D8; EMBL:U32615

Query Match 16.7%; Score 22; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.5e+04;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 ASLKQEIDALEY 21
DB 16 AEFNQQLRFLOQ 27

RESULT 5
B60071
vasoactive intestinal peptide - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998
C;Accession: B60071
R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.
Regul. Pept. 32, 39-45, 1991
A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.
A;Reference number: A60071; MUID:91164506; PMID:2003150
A;Accession: B60071
A;Status: protein sequence not shown
A;Molecule type: protein
A;Residues: 1-28 <YUA>
A;Cross-references: UNIPARC:UPI000002D1C0
A;Note: the sequence is identical with the human sequence
C;Superfamily: Glucagon
C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 15.9%; Score 21; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 2e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 QEIDALEYEND 24
DB 18 QKVDLREGERE 28

RESULT 8
PC1162
cytochrome-c oxidase (EC 1.9.3.1) chain III - goldfish mitochondrion (fragment)
C;Species: mitochondrion Carassius auratus (goldfish)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1162
R;Peng, G.; Taylor, J.D.; Tchen, T.T.
Biochem. Biophys. Res. Commun. 189, 445-449, 1992
A;Title: Increased mitochondrial activities in pigmented (melanized) fish cells and nuclei
A;Reference number: JC1348; MUID:93080595; PMID:1280425
```

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Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKQEIDALEYENDAL 26
DB 4 AVFTDNYTLRQKQMAVKYLSIL 27

RESULT 6
A60304
vasoactive intestinal peptide - dog
N;Alternate names: VIP
C;Species: Canis lupus familiaris (dog)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
C;Accession: A60304
R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.
Regul. Pept. Suppl. 3, S14, 1985
A;Title: Purification and sequencing of dog and guinea pig VIP's.
A;Reference number: A60304
A;Accession: A60304
A;Molecule type: protein
A;Residues: 1-28 <ENG>
A;Cross-references: UNIPROT:P04565; UNIPARC:UPI000002D1C0
C;Superfamily: glucagon
C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 15.9%; Score 21; DB 2; Length 28;
Best Local Similarity 20.8%; Pred. No. 2e+04;
Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKQEIDALEYENDAL 26
DB 4 AVFTDNYTLRQKQMAVKYLSIL 27

RESULT 7
G69384
conserved hypothetical protein AFL079 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69384
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69384
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <KLE>
A;Cross-references: UNIPROT:O29184; UNIPARC:UPI0000056E69; GB:AE001028; GB:AE000782; NID:

Query Match 15.9%; Score 21; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 2e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 QEIDALEYEND 24
DB 18 QKVDLREGERE 28

RESULT 8
PC1162
cytochrome-c oxidase (EC 1.9.3.1) chain III - goldfish mitochondrion (fragment)
C;Species: mitochondrion Carassius auratus (goldfish)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1162
R;Peng, G.; Taylor, J.D.; Tchen, T.T.
Biochem. Biophys. Res. Commun. 189, 445-449, 1992
A;Title: Increased mitochondrial activities in pigmented (melanized) fish cells and nuclei
A;Reference number: JC1348; MUID:93080595; PMID:1280425
```

A;Accession: PC1162
A;Molecule type: DNA
A;Residues: 1-28 <PEN>
A;Cross-references: UNIPROT:Q9PSI6; UNIPARC:UPI000000FC513
C;Genetics:
A;Gene: fmel-3
A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 15.2%; Score 20; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 16 IDALEY 21
Db 13 LOAMEY 18

RESULT 9
A60303
vasoactive intestinal peptide - smaller spotted catshark
C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C;Accession: A60303; A60314; S07432
R;Dimoline, R.; Thwaites, D.T.; Young, J.; Lee, C.M.; Thorndyke, M.C.
Regul. Pept. 18, 356, 1987
A;Title: A novel family of VIP-like peptides from the dogfish Scyliorhinus canicula.
A;Reference number: A60303
A;Accession: A60303
A;Molecule type: protein
A;Residues: 1-28 <DIW>
A;Cross-references: UNIPROT:P09685; UNIPARC:UPI000013884B
A;Note: this reference is an abstract
R;Dimoline, R.; Thorndyke, M.C.; Young, J.
Regul. Pept. 14, 1-10, 1986
A;Title: Isolation and partial sequence of elasmobranch VIP.
A;Reference number: A60314; MUID:86234323; PMID:3715063
A;Accession: A60314
A;Molecule type: protein
A;Residues: 1-10 <DI2>
A;Cross-references: UNIPARC:UPI000017662D
R;Dimoline, R.; Young, J.; Thwaites, D.T.; Lee, C.M.; Thorndyke, M.C.
Ann. N. Y. Acad. Sci. 527, 621-623, 1988
A;Title: Amino acid sequence of a biologically active vasoactive intestinal peptide from
A;Reference number: S07432
A;Accession: S07432
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DI3>
A;Cross-references: UNIPARC:UPI000013884B
C;Superfamily: glucagon
C;Keywords: amidated carboxyl end; duplication; intestine; neuropeptide
P;28/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 15.2%; Score 20; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASL 12
Db 15 KOMAVKKYINSL 26

RESULT 10
S21742
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - rape
C;Species: Brassica napus (rape)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C;Accession: S21742
R;Sheldon, P.S.; Kekwick, R.G.O.; Smith, C.G.; Sidebottom, C.; Siabaa, A.R.
Biochim. Biophys. Acta 1120, 151-159, 1992

A;Title: 3-Oxoacyl-[ACP] reductase from oilseed rape (Brassica napus).
A;Reference number: S21742; MUID:92223071; PMID:1562581
A;Accession: S21742
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <SHE>
A;Cross-references: UNIPARC:UPI000017B028
C;Keywords: oxidoreductase

Query Match 15.2%; Score 20; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 2.6e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 17 DALEY 21
Db 1 DAVDY 5

RESULT 11
T06340
ribosomal protein S16 - soybean chloroplast (fragment)
C;Species: chloroplast Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06340
R;Nielsen, N.C.
submitted to the EMBL Data Library, May 1995
A;Reference number: Z15613
A;Accession: T06340
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <NIE>
A;Cross-references: UNIPROT:Q32307; UNIPARC:UPI000008B5A1; EMBL:U26948; NID:g984307; PID
A;Experimental source: cultivar Reenik; leaf.
C;Genetics:
A;Gene: rps16
A;Genome: chloroplast
C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 15.2%; Score 20; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 2.6e+04;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 9 IASLQKQIDALEYE 22
Db 4 IESLQSMFDLEERE 17

RESULT 12
H85908
hypothetical protein Z3917 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85908
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <STO>
A;Cross-references: UNIPROT:Q8X415; UNIPARC:UPI00000D0867; GB:AE005174; NID:g12517049; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3917

Query Match 14.8%; Score 19.5; DB 2; Length 28;
Best Local Similarity 38.1%; Pred. No. 3e+04;
Matches 8; Conservative 1; Mismatches 9; Indels 3; Gaps 1;

Qy 10 ASLKQKQID---ALEYENDALE 27

Db 7 APLQDAADLEIATEETSLE 27

RESULT 13

A32643
deoxyribodipyrimidine photo-lyase (EC 4.1.1.99.3) - Methanobacterium thermoautotrophicum
N;Alternate names: photoreactivating enzyme
C;Species: Methanobacterium thermoautotrophicum
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Apr-1999
C;Accession: A32643
R;Kiener, A.; Hsuain, I.; Sancar, A.; Walsh, C.
J. Biol. Chem. 264, 13860-13867, 1989
A;Title: Purification and properties of Methanobacterium thermoautotrophicum DNA photolyase
A;Reference number: A32643; MUID:89340481; PMID:2668276
A;Accession: A32643
A;Molecule type: protein
A;Residues: 1-28 <KTE>
A;Cross-references: UNIPARC:UPI0000131976
C;Superfamily: deoxyribodipyrimidine photo-lyase
C;Keywords: carbon-carbon lyase; DNA binding

Query Match 14.4%; Score 19; DB 2; Length 28;
Best Local Similarity 44.4%; Pred. No. 3.5e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 QKTASLKQE 15

Db 5 ERIRSLNTE 13

RESULT 14

S11618
ribosomal protein S8 [validated] - Halobacterium salinarum (fragment)
N;Alternate names: ribosomal protein HS20
C;Species: Halobacterium salinarum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S11618
R;Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982
A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea
A;Reference number: S11609
A;Accession: S11618
A;Molecule type: protein
A;Residues: 1-28 <YAG>
A;Cross-references: UNIPROT:Q7M552; UNIPARC:UPI0000177283
A;Note: the protein is designated as ribosomal protein HS20
A;Note: the source is designated as Halobacterium cutirubrum
C;Superfamily: Escherichia coli ribosomal protein S8
C;Keywords: protein biosynthesis; ribosome

Query Match 14.4%; Score 19; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 3.5e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 17 DALEYENDA 25

Db 8 DALSGIDDA 16

RESULT 15

JW0019
mast cell degranulating peptide - American common bumblebee
C;Species: Bombus pennsylvanicus (American common bumblebee)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JW0019
R;Argiolas, A.; Herring, P.; Pisano, J.J.
Peptides 6, 431-436, 1985
A;Title: Amino acid sequence of bumblebee MCD peptide: a new mast cell degranulating peptide
A;Reference number: JW0019; MUID:86177038; PMID:2421265
A;Accession: JW0019
A;Molecule type: protein
A;Residues: 1-28 <ARG>
A;Cross-references: UNIPROT:P04567; UNIPARC:UPI000012ED6C

Query Match 14.4%; Score 19; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 3.5e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 17 DALEYENDA 25

Db 8 DALSGIDDA 16

A;Experimental source: venom

C;Keywords: amidated carboxyl end; venom

F;2-18,4-22/Disulfide bonds: #status experimental

F;28/Modified site: amidated carboxyl end (His) #status predicted

Query Match 14.4%; Score 19; DB 2; Length 28;
Best Local Similarity 30.8%; Pred. No. 3.5e+04;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IAALKQKIASLKQ 14

Db 14 IGKICRKICMQQ 26

RESULT 16

I48178
orphan receptor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I48178
R;Pena de Ortiz, S.; Cannon, M.M.; Jamieson, G.A.
Brain Res. Mol. Brain Res. 23, 278-283, 1994
A;Title: Expression of nuclear hormone receptors within the rat hippocampus: identification
A;Reference number: I48178; MUID:94335560; PMID:7914660
A;Accession: I48178
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-28 <RES>
A;Cross-references: UNIPROT:Q63743; UNIPARC:UPI00000E8408; GB:L19344; NID:G349093; PIDN:1

Query Match 14.0%; Score 18.5; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 4e+04;
Matches 6; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 11 SLKQEID--ALEYEN 23

Db 6 SIQQNIQYKKLKNEN 21

RESULT 17

A34244
hexokinase (EC 2.7.1.1), pancreatic - rat (fragments)
N;Alternate names: glucokinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 03-Jun-1993 #text_change 28-Feb-1997
C;Accession: A34244
R;Magnuson, M.A.; Shelton, K.D.
J. Biol. Chem. 264, 15936-15942, 1989
A;Title: An alternate promoter in the glucokinase gene is active in the pancreatic beta
A;Reference number: A34244; MUID:89380186; PMID:2550428
A;Accession: A34244
A;Molecule type: mRNA
A;Residues: 1-28 <MAG>
A;Cross-references: UNIPARC:UPI000017553D; GB:M25807
A;Note: the authors translated the codon CTG for residue 2 as Lys
C;Superfamily: hexokinase; hexokinase homology
C;Keywords: ATP; glycolysis; phosphotransferase

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 30.0%; Pred. No. 4.5e+04;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 AALKQKIASL 12

Db 10 ATKKEKVEQI 19

RESULT 18

A60752
outer membrane protein A - Yersinia pseudotuberculosis (fragment)
N;Alternate names: heat-modifiable protein; outer membrane protein II
C;Species: Yersinia pseudotuberculosis
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 30.0%; Pred. No. 4.5e+04;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 AALKQKIASL 12

Db 10 ATKKEKVEQI 19

C;Accession: A60752
R;Zhang, J.J.; Hamachi, M.; Hamachi, T.; Zhao, Y.P.; Yu, D.T.Y.
J. Immunol. 143, 2955-2960, 1989
A;Title: The bacterial outer membrane protein that reacts with anti-HLA-B27 antibodies
A;Reference number: A60752; MUID:90038529; PMID:2478630
A;Accession: A60752
A;Molecule type: protein
A;Residues: 1-28 <ZHA>
A;Cross-references: UNIPROT:P38399; UNIPARC:UPI0000130CFC
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 4.5e+04;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 20 EYEND 24
:|::|
Db 17 QYQDD 21

RESULT 19
S07826
venom protein - American tarantula (Eurytelma californica) (fragment)
C;Species: Eurytelma californica
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S07826
R;Savel-Niemann, A.
Biol. Chem. Hoppe-Seyler 370, 485-498, 1989
A;Title: Tarantula (Eurytelma californicum) venom, a multicomponent system.
A;Reference number: S04224; MUID:89302691; PMID:2742756
A;Accession: S07826
A;Molecule type: protein
A;Residues: 1-28 <SAV>
A;Cross-references: UNIPARC:UPI000017BE06
C;Keywords: venom

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 57.1%; Pred. No. 4.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AALKQKI 9
|::|
Db 10 AGVTQKI 16

RESULT 20
S63502
95K protein - Eubacterium acidaminophilum (fragment)
C;Species: Eubacterium acidaminophilum
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S63502
R;Meyer, M.; Granderath, K.; Andreessen, J.R.
Eur. J. Biochem. 234, 184-191, 1995
A;Title: Purification and characterization of protein P(B) of betaine reductase and its
philum.

A;Reference number: S63502; MUID:96096737; PMID:8529639
A;Accession: S63502
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-28 <MEY>
A;Cross-references: UNIPROT:Q9R4G6; UNIPARC:UPI00000B2F3E

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 15 EIDALEYE 22
:|::|
Db 5 KIDGRELE 12

RESULT 21

S16228
aryl acylamidase - Nocardia globnerula
C;Species: Nocardia globnerula
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
A;Accession: S16228
R;Yoshioka, H.; Nagasawa, T.; Yamada, H.
Eur. J. Biochem. 199, 17-24, 1991
A;Title: Purification and characterization of aryl acylamidase from Nocardia globnerula.
A;Reference number: S16228; MUID:91293120; PMID:2065673
A;Accession: S16228
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <EUR>
A;Cross-references: UNIPROT:P80008; UNIPARC:UPI000001260D8

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 16 IDALEY 21
:|::|
Db 1 MDVAEY 6

RESULT 22

S66436
allophycocyanin alpha-B chain - Anabaena sp. (strain PCC 7120) (fragment)
C;Species: Anabaena sp.
A;Variety: PCC 7120
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66436
R;Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.
Eur. J. Biochem. 236, 1010-1024, 1996
A;Title: Isolation, characterization and electron microscopy analysis of a hemidiscoidal
A;Reference number: S66435; MUID:96270757; PMID:8665889
A;Accession: S66436
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DUC>
A;Cross-references: UNIPROT:P80556; UNIPARC:UPI0000174E0E
C;Superfamily: phycocyanin

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 14 QEIDALEY 21
|::|
Db 9 QADDELY 16

RESULT 23

S47624
D-aspartate oxidase (EC 1.4.3.1) - common octopus (fragment)
C;Species: Octopus vulgaris (common octopus)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 07-May-1999
C;Accession: S47624
R;Tedeschi, G.; Negri, A.; Cecilian, F.; Roñchi, S.; Vetere, A.; D'Aniello, G.; D'Aniel
Biochim. Biophys. Acta 1207, 217-222, 1994
A;Title: Properties of the flavoenzyme D-aspartate oxidase from Octopus vulgaris.
A;Reference number: S47624; MUID:94355383; PMID:7915543
A;Accession: S47624
A;Molecule type: protein
A;Residues: 1-28 <TED>
A;Cross-references: UNIPARC:UPI000017502F
A;Experimental source: hepatopancreas
C;Function:

A;Description: this enzyme is a flavoprotein that catalyzes the oxidative deamination of
A;Superfamily: D-amino-acid oxidase
C;Keywords: oxidoreductase; monomer; blocked amino end; FAD

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 5.9e+04;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIAA0KQIASL 12
||| : : |
Db 2 KIAVIGVVGL 13

RESULT 24

JX0059
serine proteinase inhibitor MCEI-I - balsam pear
C;Species: Momordica charantia (Balsam pear, bitter melon)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JX0059
R;Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A;Title: Amino acid sequences and disulfide bridges of serine proteinase inhibitors from
A;Reference number: JX0057; MUID:89291812; PMID:2738047
A;Accession: JX0059
A;Molecule type: protein
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPROT:P10296; UNIPARC:UPI000012D226
C;Superfamily: squash trypsin inhibitor ITD I
C;Keywords: serine proteinase inhibitor
F;3-20,10-22,16-27/Disulfide bonds: #status predicted

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 22 ENDALQ 28
: : : : |
Db 13 DSDCLAQ 19

RESULT 25

A38232
vasoactive intestinal peptide - North American opossum
N;Alternate names: VIP
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A38232
R;Eng, J.; Yu, J.; Rattan, S.; Yalow, R.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 1809-1811, 1992
A;Title: Isolation and amino acid sequences of opossum vasoactive intestinal polypeptide
A;Reference number: A38232; MUID:92179271; PMID:1542675
A;Accession: A38232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <ENG>
A;Cross-references: UNIPROT:P39089; UNIPARC:UPI0000138846
A;Note: sequence extracted from NCBI backbone (NCBIP:87215)
C;Superfamily: glucagon
C;Keywords: duplication, intestine; neuropeptide

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 26.7%; Pred. No. 5.9e+04;
Matches 4; Conservative 7; Mismatches 2; Indels 2; Gaps 1;

QY 5 LKQKIASLKQEIDAL 19
||| : : : : |
Db 14 LKQ--MAMRKYLDLSI 26

RESULT 26

S72460
ribosomal protein S19 - curled-leaved tobacco chloroplast (fragment)
C;Species: chloroplast Nicotiana glauca plumbaginifolia (curled-leaved tobacco)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S72460
R;Goulding, S.E.; Olmstead, R.G.; Morden, C.W.; Wolfe, K.H.
Mol. Gen. Genet. 252, 195-206, 1996

A;Title: Ebb and flow of the chloroplast inverted repeat.
A;Reference number: S72459; MUID:96397499; PMID:8804393
A;Accession: S72460
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <GOU>

A;Cross-references: UNIPROT:Q36593; UNIPARC:UPI000008D033; EMBL:Z71241; NID:gl279593; PII
A;Note: only a part of the nucleic acid sequence is shown
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
C;Genetics:

A;Gene: rps19
A;Genome: chloroplast
A;Start codon: GTG
C;Function:
A;Pathway: protein biosynthesis
C;Superfamily: ribosomal protein S19/S15
C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.9e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LKQEIDAL 19
| : : : |
Db 15 LKKIDKL 22

RESULT 27

A23691
apolipoprotein C-I - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C;Accession: A23691
R;Weisgraber, K.H.; Mahley, R.W.; Kowal, R.C.; Herz, J.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 265, 22453-22459, 1990
A;Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-migrator
ceptor-related protein.
A;Reference number: A23691; MUID:91093092; PMID:2266137

A;Accession: A23691
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <WEI>
A;Cross-references: UNIPROT:P33047; UNIPARC:UPI0000125C1C
C;Superfamily: apolipoprotein A-I
C;Keywords: lipid binding; lipoprotein

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 28.6%; Pred. No. 5.9e+04;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 15 BIDALEYENDALEQ 28
: : : : :
Db 3 DFSTLELIQDLKE 16

RESULT 28

S56746
alpha-synuclein, NAC - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S56746
R;Jensen, P.H.; Sorensen, E.S.; Petersen, T.E.; Gliemann, J.; Rasmussen, L.K.
Biochem. J. 310, 91-94, 1995
A;Title: Residues in the synuclein consensus motif of the alpha-synuclein fragment, NAC.
A;Reference number: S56746; MUID:95374478; PMID:7646476
A;Accession: S56746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <JEN>
A;Cross-references: UNIPARC:UPI0000179D22

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 5.9e+04;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IAALKQK 8
: | : |
Db 15 VTAVAQK 21

RESULT 29

S38524
rRNA N-glycosidase (EC 3.2.2.22) saporin R1 - common soapwort (fragment)
C:Species: Saponaria officinalis (common soapwort)
C>Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: S38524
R:Ferreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; Roc
Biochim. Biophys. Acta 1216, 31-42, 1993
A:Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA
A:Reference number: S38521; MUID:94032486; PMID:8218413
A:Accession: S38524
A:Molecule type: Protein
A:Residues: 1-28 <PER>
A:Cross-references: UNIPROT:Q7MI18; UNIPARC:UPI000017AF39
C:Keywords: glycosidase; hydrolase

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 19 LEYENDA 25
: | : |
Db 8 LEFGQDS 14

RESULT 30

PC4430
peroxisome proliferator activated receptor gamma variant, P12A - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C:Accession: PC4430
R:Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A:Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
A:Reference number: PC4429; MUID:98086341; PMID:9425261
A:Accession: PC4430
A:Molecule type: DNA
A:Residues: 1-28 <YEN>
A:Cross-references: UNIPARC:UPI000017A1D0
C:Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
C:Genetics:
A:Introns: 28/1

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 ASLKQK 15
: | : |
Db 23 ANISQK 28

RESULT 31

PC4429
peroxisome proliferator activated receptor gamma - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C:Accession: PC4429
R:Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A:Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
A:Reference number: PC4429; MUID:98086341; PMID:9425261
A:Accession: PC4429
A:Molecule type: DNA
A:Residues: 1-28 <YEN>
A:Cross-references: UNIPARC:UPI000017A1CF

C:Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
C:Genetics:
A:Introns: 28/1

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 ASLKQK 15
: | : |
Db 23 ANISQK 28

RESULT 32

A31859
deoxycytidine kinase (EC 2.7.1.74) / deoxyadenosine kinase (EC 2.7.1.76) - Lactobacillus
C:Species: Lactobacillus acidophilus
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C:Accession: A31859
R:Ikedu, S.; Swenson, R.P.; Ives, D.H.
Biochemistry 27, 8648-8652, 1988
A:Title: Amino-terminal nucleotide-binding sequences of a Lactobacillus deoxynucleoside
A:Reference number: A31859; MUID:89118283; PMID:2851331
A:Accession: A31859
A:Molecule type: protein
A:Residues: 1-28 <IKS>
A:Cross-references: UNIPROT:Q7M0X4; UNIPARC:UPI00000175695
A:Note: 18-Ile, 21-Lys, 26-Gln, and 27-Ala were also found
C:Keywords: phosphotransferase

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 5.9e+04;
Matches 5; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IAALKQKIASLKQK 15
: | : |
Db 8 IGAGKSSLTGLLAE 21

RESULT 33

T47196
RAS protein [imported] - Neurospora crassa (fragment)
C:Species: Neurospora crassa
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47196
R:Lee, C.W.; Lee, E.
A:Description: Structural analysis of ras genes from filamentous fungi.
A:Reference number: Z24384
A:Accession: T47196
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <LEE>
A:Cross-references: UNIPROT:P22126; UNIPARC:UPI000016891F; EMBL:U33746; PIDN:AAA74986.1
C:Genetics:
A:Gene: ras
A:Note: Intron positions not resolved (incomplete sequence)
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 21.4%; Pred. No. 7.6e+04;
Matches 3; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 7 QKIASLKQKSIDALE 20
: | : |
Db 4 RKQCTIDNEVALLD 17

RESULT 34

PH0231
T-cell receptor Vb CDR3, carrier PBL Vb 6.sbt - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 30-May-1997

```

Qy      13 KQEIDALEYEN 23
      :|::|
Db      1 EQLVNVTELN 11

RESULT 37
PS0106
2-phosphinomethylmalic acid synthase - Streptomyces hygroscopicus (fragment)
N:Alternate names: PMM synthase
C:Species: Streptomyces hygroscopicus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: PS0106
R:Shimotohno, K.W.; Imai, S.; Murakami, T.; Seto, H.
Agric. Biol. Chem. 54, 463-470, 1990
A:Title: Purification and characterization of citrate synthase from Streptomyces hygroscopicus
A:Reference number: PS0106; MUID:90334852; PMID:1368511
A:Accession: PS0106
A:Molecule type: DNA
A:Residues: 1-28 <SHI>
A:Cross-references: UNIPROT:Q9LCB4; UNIPROT:Q03618; UNIPARC:UPI000017AE21
A:Experimental source: Strain SF-1293
C:Comment: This enzyme catalyzes the condensation reaction between phosphinopyruvic acid and pyruvate.

Query Match      12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      21 YENDALEQ 28
      :|||
Db      16 FPQDAFPQ 23

RESULT 38
A69259
Hypothetical protein AF0073 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69259
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69259
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-28 <KLS>
A:Cross-references: UNIPROT:Q30163; UNIPARC:UPI0000057244; GB:AE001101; GB:AE000782; NID

Query Match      12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      13 KQEID 17
      :|||
Db      16 RAEID 20

RESULT 39
T09594
gene LFY protein - Monterey pine (fragment)
C:Species: Pinus radiata (Monterey pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09594
R:Izquierdo, L.V.; Vergara, R.F.; Alvarez-Buylla, E.R.
submitted to the EMBL Data Library, August 1996
A:Description: Partial characterization of Pinus radiata meristem identity homolog gene
A:Reference number: Z16756
A:Accession: T09594
A:Status: preliminary; translated from GB/EMBL/DDJF

```


A:Molecule type: DNA
A:Residues: 1-28 <I20>
A:Cross-references: UNIPROT:O24285; UNIPARC:UPI000000AC880; EMBL:U66725; NID:gl513305; PID:
C:Species: Homo sapiens (man)
C:Genetics:
A:Gene: LFY
C:Function:
A:Description: controls meristem identity

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 7.6e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ALKQK 8
||:|
Db 14 ALRKK 18

RESULT 40
I68614
frame shifted FMR1 exon - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: I68614; I68615
R:Richier, E.E.; Richards, S.; Gibbs, R.A.; Nelson, D.L.
Hum. Mol. Genet. 2, 1147-1153, 1993
A:Title: Fine structure of the human FMR1 gene.
A:Reference number: I54334; MUID:94004853; PMID:8401496
A:Accession: I68614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <E11>
A:Cross-references: UNIPROT:Q16578; UNIPARC:UPI0000006DB1C; GB:L19490; NID:g388747; PIDN:
A:Accession: I68615
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <E12>
A:Cross-references: UNIPARC:UPI0000006DB1C; GB:L19491; NID:g388749; PIDN:AAA62467.1; PID:
C:Comment: This sequence appears to be the frame shifted hypothetical translation of an
C:Genetics:
A:Gene: GDB:FMR1
A:Cross-references: GDB:I29038; OMIM:309550
A:Map position: Xq27.3-Xq27.3

Query Match 12.1%; Score 16; DB 4; Length 28;
Best Local Similarity 75.0%; Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LKQE 15
||:|
Db 18 LKEE 21

RESULT 41
T14210
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Uromastix acanthinurus mitochondrion
C:Species: mitochondrion Uromastix acanthinurus
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14210
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826; PMID:9000757
A:Accession: T14210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <MAC>
A:Cross-references: UNIPROT:P92760; UNIPARC:UPI0000099123; EMBL:U71325; NID:gl753264; PID:
A:Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology, University
C:Genetics:
A:Gene: mitochondrion
A:Note: NDI
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 30.8%; Pred. No. 9.6e+04;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 11 SLKQEIDALEYEN 23
||:|
Db 15 NLPSALALPPDN 27

RESULT 42
T12301
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Diposaurus dorsalis mitochondrion
C:Species: mitochondrion Diposaurus dorsalis
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12301
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example using
A:Reference number: Z17488; MUID:99162288; PMID:10051389
A:Accession: T12301
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <SCH>
A:Cross-references: UNIPROT:Q92YV5; UNIPARC:UPI000008FBBF; EMBL:AF049857; NID:g4105726;
A:Experimental source: specimen voucher Museum of Vertebrate Zoology, Berkeley, California
C:Genetics:
A:Gene: mitochondrion
A:Note: NDI
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 9.6e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 11 SLKQEIDAL 19
||:|
Db 15 SLPTSIFAL 23

RESULT 43
A60291
24K proteinase (EC 3.4.-.-) - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 15-Oct-1999
C:Accession: A60291
R:Ikedo, M.; Sasaki, T.; Yamashita, O.
Insect Biochem. 20, 725-734, 1990
A:Title: Purification and characterization of proteases responsible for vitellin degradation
A:Reference number: A60291
A:Accession: A60291
A:Molecule type: protein
A:Residues: 1-28 <IKE>
A:Cross-references: UNIPARC:UPI0000175C3C
A:Comment: This enzyme degrades the nutritional yolk protein vitellin during embryogenesis
C:Superfamily: trypsin; trypsin homology
C:Keywords: egg yolk; hydrolase

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 9.6e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AALKQKTASL 12
||:|
Db 19 ASMXNXIAL 28

RESULT 44
S55729
orotidine-5'-monophosphate decarboxylase - Aspergillus awamori (fragments)
C:Species: Aspergillus awamori
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004

C;Accession: S55729
R;Gouka, R.J.; Heesing, J.G.M.; Stam, H.; Musters, W.; van den Hondel, C.A.M.J.J.
Curr. Genet. 27, 536-540, 1995
A;Title: A novel strategy for the isolation of defined pyrG mutants and the development
A;Reference number: S55729; MUID:96031709; PMID:7553938
A;Accession: S55729
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18;19-28 <GOU>
A;Cross-references: UNIPARC:UPI0000069725; UNIPARC:UPI0000175F90
C;Superfamily: Orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylase

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 22.2%; Pred. No. 9.6e+04;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 IASLKOEID 17

Db 7 VTTKELLD 15

RESULT 45

JX0058
trypsin inhibitor MCTI-II - balsam pear
C;Species: Momordica charantia (balsam pear, bitter melon)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JX0058
R;Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A;Title: Amino acid sequences and disulfide bridges of serine proteinase inhibitors from
A;Reference number: JX0057; MUID:89291812; PMID:2738047
A;Accession: JX0058
A;Molecule type: protein
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPROT:P10295; UNIPARC:UPI000012DA53
C;Superfamily: squash trypsin inhibitor ITD I
C;Keywords: serine proteinase inhibitor
F;3-20,10-22,16-27/Disulfide bonds: #status experimental

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 28.6%; Pred. No. 9.6e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 22 ENDALEQ 28

Db 13 DSDCMAQ 19

Search completed: November 21, 2005, 21:47:32
Job time : 25.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:26:34 ; Search time 142 Seconds
(without alignments)
139.118 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQIDALEDVENDALBQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1678

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	24.2	28	Q8ZYV3 PYRAE	Q8ZYV3 pyrobaculum
2	31	23.5	28	Q4YLJ0 PLABE	Q4YLJ0 plasmodium
3	30	22.7	28	Q63111 ARATH	Q63111 arabidopsis
4	28	21.2	28	Q9RAT7 LACLC	Q9RAT7 lactococcus
5	26	19.7	28	Q4TIF5 TETNG	Q4TIF5 tetraodon n
6	25.5	19.3	28	Q7S0D5 NEUCR	Q7S0D5 neurospora
7	25	18.9	28	Q7XU72 ORYSA	Q7XU72 oryza sativ
8	25	18.9	28	Q9XGE4 VICFA	Q9XGE4 vicia faba
9	25	18.9	28	Q80KE6 9RHAB	Q80KE6 rabies viru
10	25	18.9	28	Q6DQ01 9RHAB	Q6DQ01 rabies viru
11	24.5	18.6	28	Q38269 LAMBQ	Q38269 bacterioph
12	24.5	18.6	28	Q5PF48 SALPA	Q5PF48 salmoneilla
13	24	18.2	28	Q9URD3 ASPOR	Q9URD3 aspergillus
14	24	18.2	28	Q6B3M0 DROPHI	Q6B3M0 drosophila
15	24	18.2	28	Q9TXX0 MANSE	Q9TXX0 manduca sex
16	24	18.2	28	Q4XF30 PLACH	Q4XF30 plasmodium
17	24	18.2	28	Q4YLJ2 PLABE	Q4YLJ2 plasmodium
18	23	17.4	28	Q4X244 ASPFU	Q4X244 aspergillus
19	23	17.4	28	Q4XER1 PLACH	Q4XER1 plasmodium
20	23	17.4	28	Q4YA03 PLABE	Q4YA03 plasmodium
21	23	17.4	28	Q62731 CANFA	Q62731 canis faml
22	23	17.4	28	Q80KK2 9RHAB	Q80KK2 rabies viru
23	23	17.4	28	Q80KL1 9RHAB	Q80KL1 rabies viru
24	23	17.4	28	Q80KL4 9RHAB	Q80KL4 rabies viru
25	23	17.4	28	Q6DQP6 9RHAB	Q6DQP6 rabies viru
26	23	17.4	28	Q6DQ03 9RHAB	Q6DQ03 rabies viru
27	22	16.7	28	Q9NCS6 TRYCR	Q9NCS6 trypanosoma
28	22	16.7	28	Q4X811 PLACH	Q4X811 plasmodium
29	22	16.7	28	Q4YAC7 PLABE	Q4YAC7 plasmodium
30	22	16.7	28	Q4YLX3 PLABE	Q4YLX3 plasmodium
31	22	16.7	28	Q704W4 BOVIN	Q704W4 bos taurus

32	22	16.7	28	2	Q71KP5 SPIMX	Q71kp5 spirogyra m
33	22	16.7	28	2	Q9R4V6 RENSA	Q9r4v6 renibacteri
34	22	16.7	28	2	Q5F210 MOUSE	Q5f210 mus musculu
35	22	16.7	28	2	Q80KF1 9RHAB	Q80kfl rabies viru
36	22	16.7	28	2	Q80KG5 9RHAB	Q80kgs rabies viru
37	22	16.7	28	2	Q9PRN8 CARAU	Q9prn8 carassius a
38	22	16.7	28	2	Q4RLC7 TETNG	Q4rlc7 tetraodon n
39	22	16.7	28	2	Q4SFN6 TETNG	Q4sfns tetraodon n
40	22	16.7	28	2	Q4T3N5 TETNG	Q4t3ns tetraodon n
41	21.5	16.3	28	2	Q4XPA5 PLACH	Q4xpa5 plasmodium
42	21	15.9	28	1	MT2 BRANA	Q96353 brassica na
43	21	15.9	28	1	VI03 VACCP	Q00334 vaccinia vi
44	21	15.9	28	1	VIP CANFA	P63289 canis faml
45	21	15.9	28	1	VIP CAPHI	P63290 capra hircu

ALIGNMENTS

RESULT 1

ID	Q8ZYV3 PYRAE	PRELIMINARY;	PRT;	28 AA.
AC	Q8ZYV3;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-JUN-2003 (Tremblrel. 24, Last annotation update)			
DE	Hypothetical protein PAE0551.			
GN	OrderedLocustNames=PAE0551;			
OS	Pyrobaculum aerophilum.			
OC	Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;			
OC	Thermoproteaceae; Pyrobaculum.			
OX	NCBI_TaxID=13773;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=IM2 / ATCC 51768 / DSM 7523;			
RX	MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;			
RA	Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,			
RA	Miller J.H.;			
RT	"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum			
RT	aerophilum.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).			
DR	EMBL; AE009773; AAL62858.1; -; Genomic DNA.			
KW	Complete proteome; Hypothetical protein.			
SQ	SEQUENCE 28 AA; 3001 MW; 869F81422C53A14D CRC64;			

Query Match 24.2%; Score 32; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 8.8e+03;
Matches 6; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy	2	IAALKOKIASLKQSIDAL 19
Db	3	VAEIKASVAELKVGSL 20

RESULT 2

ID	Q4YLJ0 PLABE	PRELIMINARY;	PRT;	28 AA.
AC	Q4YLJ0;			
DT	13-SEP-2005 (Tremblrel. 31, Created)			
DT	13-SEP-2005 (Tremblrel. 31, Last sequence update)			
DT	13-SEP-2005 (Tremblrel. 31, Last annotation update)			
DE	Hypothetical protein (Fragment).			
GN	ORFNames=PB400925.00.0;			
OS	Plasmodium Berghiei.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_TaxID=5821;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,			
RA	Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,			
RA	James K., Rutherford K., Harris B., Harris D., Churcher C.,			
RA	Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,			
RA	Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,			

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RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcripomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01003874; CAI01121.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3516 MW; 1A2DFD1935C265AE CRC64;

Query Match 23.5%; Score 31; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 1.2e+04;
Matches 5; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 KOKIASLKQEI DALEYEND 24
Db 2 KQLLKIEMRKDGCRYHE 20

RESULT 3
O65311 ARATH
ID O65311 ARATH PRELIMINARY; PRT; 28 AA.
AC O65311;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Beta-9 tubulin (Fragment).
GN Name=TUB9;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sanders P.M., Bui A.Q., Meterings K., McIntire K.N., Hau Y.C.,
RA Lee P.Y., Truong M.T., Beals T.B., Goldberg R.B.;
RT "Another Development Defects in Arabidopsis thaliana Male-Sterile
RT Mutants.";
RL Sex. Plant Reprod. 11:297-322(1999).
DR EMBL; AF060248; AAC97107.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 28 AA; 3388 MW; 8060E4E537BE670E CRC64;

Query Match 22.7%; Score 30; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.5e+04;
Matches 9; Conservative 3; Mismatches 8; Indels 4; Gaps 1;

QY 9 IASLKQEI DAL---EYENDALEQ 28
Db 3 VAEVQVQDATTGVEEVEEEDDEE 26

RESULT 4
Q9RAT7 LACIC
ID Q9RAT7 LACIC PRELIMINARY; PRT; 28 AA.
AC Q9RAT7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE DNA ligase homolog (Fragment).
GN Name=lig;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Petersen A., Josephsen J., Johnsen M.G.;
RL "fW22, a lactococcal temperate phage with a site-specific integrate

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RT closely related to Streptococcus thermophilus phage integrases.";
RL J. Bacteriol. 181:7034-7042(1999).
DR EMBL; AF065985; AAF13028.1; -; Genomic_DNA.
DR GO; GO:0003911; F:DNA ligase (NAD+) activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR001679; DNAligase.
DR Pfam; PF01653; DNA_ligase_aden; 1.
KW Ligase.
FT NON TER 28
SQ SEQUENCE 28 AA; 3418 MW; 532F398A7706A580 CRC64;

Query Match 21.2%; Score 28; DB 2; Length 28;
Best Local Similarity 20.8%; Pred. No. 2.7e+04;
Matches 5; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 5 LKQIASLKQEI DALEYENDALEQ 28
Db 3 IESKKEFTDQLNQFAIEYITLDE 26

RESULT 5
Q4TIF5 TETNG
ID Q4TIF5_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4TIF5;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF2190, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00038313001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutacheau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crallius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAR01002190; CAF87327.1; -; Genomic_DNA.
FT NON TER 28
SQ SEQUENCE 28 AA; 3040 MW; 776D95631570A999 CRC64;

Query Match 19.7%; Score 26; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 4.7e+04;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 AALKQKIASLKQEI 16
Db 11 AEVRAKLAELELEL 24

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RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL662998; CAD41522.2; -; Genomic_DNA.
DR Gramene; Q7XU72; -.
SQ SEQUENCE 28 AA; 3150 MW; 715B4E08C513DCD3 CRC64;

Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 6.1e+04;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 ASLKQIDALEYEN 23
   |||:|:|:|
DB 13 ASLMELEGKIFWN 26

RESULT 8
Q9XGE4 VICFA
ID Q9XGE4 VICFA PRELIMINARY; PRT; 28 AA.
AC Q9XGE4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ribonuclease H (Fragment).
DE Name=RNase H;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pearce S.R., Stuart-Rogers C., Knox M., Kumar A., Ellis T.H.,
RA Flavell A.J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243103; CAB45147.1; -; Genomic_DNA.
DR InterPro; IPR000886; ER_target_S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 28 AA; 3187 MW; 1213C2C39C722B7C CRC64;

Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.1e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 IDALEYEN 23
   |||:|:|
DB 8 LDANQFEN 15

RESULT 9
Q80KE6 9RHAB
ID Q80KE6 9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KE6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; aRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paez A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192396; AAO45871.1; -; Genomic_RNA.
FT NON_TER

us-10-088-417a-1.rup
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL662998; CAD41522.2; -; Genomic_DNA.
DR Gramene; Q7XU72; -.
SQ SEQUENCE 28 AA; 3150 MW; 715B4E08C513DCD3 CRC64;

Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 6.1e+04;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 ASLKQIDALEYEN 23
   |||:|:|:|
DB 13 ASLMELEGKIFWN 26

RESULT 8
Q9XGE4 VICFA
ID Q9XGE4 VICFA PRELIMINARY; PRT; 28 AA.
AC Q9XGE4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ribonuclease H (Fragment).
DE Name=RNase H;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pearce S.R., Stuart-Rogers C., Knox M., Kumar A., Ellis T.H.,
RA Flavell A.J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243103; CAB45147.1; -; Genomic_DNA.
DR InterPro; IPR000886; ER_target_S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 28 AA; 3187 MW; 1213C2C39C722B7C CRC64;

Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.1e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 IDALEYEN 23
   |||:|:|
DB 8 LDANQFEN 15

RESULT 9
Q80KE6 9RHAB
ID Q80KE6 9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KE6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; aRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paez A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192396; AAO45871.1; -; Genomic_RNA.
FT NON_TER

us-10-088-417a-1.rup
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL662998; CAD41522.2; -; Genomic_DNA.
DR Gramene; Q7XU72; -.
SQ SEQUENCE 28 AA; 3150 MW; 715B4E08C513DCD3 CRC64;

Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 6.1e+04;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 ASLKQIDALEYEN 23
   |||:~:~:~
DB 13 ASLMELEGKIFWN 26

RESULT 8
Q9XGE4 VICFA
ID Q9XGE4 VICFA PRELIMINARY; PRT; 28 AA.
AC Q9XGE4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ribonuclease H (Fragment).
DE Name=RNase H;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pearce S.R., Stuart-Rogers C., Knox M., Kumar A., Ellis T.H.,
RA Flavell A.J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243103; CAB45147.1; -; Genomic_DNA.
DR InterPro; IPR000886; ER_target_S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 28 AA; 3187 MW; 1213C2C39C722B7C CRC64;

Query Match 19.3%; Score 25.5; DB 2; Length 28;
Best Local Similarity 53.8%; Pred. No. 5.3e+04;
Matches 7; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 14 QEIDAL-EYENDA 25
   |||:~:~:~
DB 9 QEVPAGSGYENRA 21

RESULT 7
Q7XU72 ORYSA
ID Q7XU72 ORYSA PRELIMINARY; PRT; 28 AA.
AC Q7XU72;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNB0020011.9 protein.
GN Name=OSJNB0020011.9;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
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SQ SEQUENCE 28 AA; 3068 MW; 2F7337A9AAC95C6A CRC64;
Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. NO. 6.1e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 16 IDALEYENDALE 27
|| : || || |
DB 12 IDPIESEADPRE 23

RESULT 10
Q6DQ01_9RHAB
ID G6DQ01_9RHAB PRELIMINARY; PRT; 28 AA.
AC G6DQ01;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Polymerase (Fragment).
GN NamesL;
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C52/98;
RA Paez A., Saad C., Nunez C., Boshell J.;
RT "Molecular epidemiology of rabies in northern Colombia 1994-2003:
RT evidence for human and fox rabies associated with dogs.";
RL Epidemiol. Infect. 133:529-536(2005).
DR EMBL; AV649921; AAT66971.1; -; Genomic_RNA.
FT NON TER 28
SQ SEQUENCE 28 AA; 3068 MW; 2F7337A9AAC95C6A CRC64;
Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. NO. 6.1e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 16 IDALEYENDALE 27
|| : || || |
DB 12 IDPIESEADPRE 23

RESULT 11
Q38269_LAMBD
ID Q38269_LAMBD PRELIMINARY; PRT; 28 AA.
AC Q38269;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf28.
OS Bacteriophage lambda.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=78234064; PubMed=354508;
RX DOI=10.1146/annurev.bi.47.070178.004535;
RA Adhya S., Gottesman M.;
RT "Control of transcription termination.";
RL Annu. Rev. Biochem. 47:967-996(1978).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83189071; PubMed=6221115;
RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
RT "Nucleotide sequence of bacteriophage lambda DNA.";
RL J. Mol. Biol. 162:729-773(1982).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=73215915; PubMed=4515613;
RA Weigel P.H., Englund P.T., Murray K., Old R.W.;

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RT "The 3'-terminal nucleotide sequences of bacteriophage lambda DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 70:1151-1155(1973).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82059489; PubMed=6458018;
RA Ieichen K., Shepherd J.C.W., Bickle T.A.;
RT "The DNA sequence of the phage lambda genome between PL and the gene
RT bet.";
RL Nucleic Acids Res. 9:4639-4653(1981).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84170247; PubMed=6324174;
RA Hohn B.;
RT "DNA sequences necessary for packaging of bacteriophage lambda DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7456-7460(1983).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85074479; PubMed=6096022; DOI=10.1016/0092-8674(84)90478-1;
RA Craig N.L., Nash H.A.;
RT "E. coli integration host factor binds to specific sites in DNA.";
RL Cell 39:707-716(1984).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85083055; PubMed=6096550;
RA Edling T.D., Cooley T.E., Richards S.H., Ihler G.M.;
RT "Long range base-pairing in the leftward transcription unit of
RT bacteriophage lambda. Characterization by electron microscopy and
RT computer-aided sequence analysis.";
RL J. Mol. Biol. 179:351-365(1984).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85083885; PubMed=6096564;
RA Frackman S., Siegele D.A., Feiss M.;
RT "A functional domain of bacteriophage lambda terminase for prohead
RT binding.";
RL J. Mol. Biol. 180:283-300(1984).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85134899; PubMed=6241264;
RA Place N., Fien K., Mahoney M.E., Wulff D.L., Ho Y.S., Debouck C.,
RA Rosenberg M., Shih M.C., Gussin G.N.;
RT "Mutations that alter the DNA binding site for the bacteriophage
RT lambda cII protein and affect the translation efficiency of the cII
RT gene.";
RL J. Mol. Biol. 180:865-880(1984).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84119525; PubMed=6229793;
RA Wulff D.L., Mahoney M., Shatzman A., Rosenberg M.;
RT "Mutational analysis of a regulatory region in bacteriophage lambda
RT that has overlapping signals for the initiation of transcription and
RT translation.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:555-559(1984).
RN [11]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84222010; PubMed=6233610;
RA Warren F., Das A.;
RT "Formation of termination-resistant transcription complex at phage
RT lambda nut locus: effects of altered translation and a ribosomal
RT mutation.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3612-3616(1984).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85232076; PubMed=2408965; DOI=10.1016/0378-1119(85)90139-8;
RA Coleclough C., Erlitz F.L.;
RT "Use of primer-restriction-end adapters in a novel cDNA cloning
RT strategy.";
RL Gene 34:305-314(1985).
RN [13]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85142185; PubMed=3156406;
RA Peltz S.W., Brown A.L., Hasan N., Podhajek A.J., Szybalski W.;
RT "Thermosensitivity of a DNA recognition site: activity of a truncated

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DR EMBL; AY687253; AAT90656.1; -; Genomic DNA.
DR EMBL; AY687251; AAT90654.1; -; Genomic DNA.
DR EMBL; AY687250; AAT90653.1; -; Genomic DNA.
DR EMBL; AY687246; AAT90649.1; -; Genomic DNA.
DR EMBL; AY687193; AAT90596.1; -; Genomic DNA.
DR EMBL; AY687279; AAT90682.1; -; Genomic DNA.
DR EMBL; AY687278; AAT90681.1; -; Genomic DNA.
DR EMBL; AY687273; AAT90676.1; -; Genomic DNA.
DR EMBL; AY687271; AAT90674.1; -; Genomic DNA.
DR EMBL; AY687233; AAT90636.1; -; Genomic DNA.
DR EMBL; AY687229; AAT90632.1; -; Genomic DNA.
DR EMBL; AY687226; AAT90629.1; -; Genomic DNA.
DR EMBL; AY687218; AAT90621.1; -; Genomic DNA.
DR EMBL; AY687211; AAT90614.1; -; Genomic DNA.
DR EMBL; AY687207; AAT90610.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004616; F:phosphoglucanate dehydrogenase (decarboxyla. .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3130 MW; 79BEB7C173784FC CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 8.1e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 SLKQEIDALE 20
Db 7 SLKDMVDK 16

RESULT 15
Q9TXX0 MANSE
ID Q9TXX0 MANSE PRELIMINARY; PRT; 28 AA.
AC Q9TXX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cell surface protein 295 91 kDa component (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingoidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92331807; PubMed=1628754;
RA Nardi J.B.;
RT "Dynamic expression of a cell surface protein during rearrangement of
RT epithelial cells in the Manduca wing monolayer."
RL Dev. Biol. 152:161-171(1992).
DR PIR; A44877; A44877.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3271 MW; 28D250E730958651 CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 8.1e+04;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 12 LKQEIDALEYEN 23
Db 14 VKQIESFEVIN 25

RESULT 16
Q4XF30 PLACH
ID Q4XF30 PLACH PRELIMINARY; PRT; 28 AA.
AC Q4XF30;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).

GN ORFNames=PC402326.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01006830; CAH84488.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3456 MW; A553FF68D5BA9A08 CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 8.1e+04;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 LKQKIASLK 13
Db 12 LRKKINTLK 20

RESULT 17
Q4YLJ2 PLABE
ID Q4YLJ2 PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YLJ2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB400921.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAI01003873; CAI01119.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3293 MW; EB2333D901B77433 CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 30.8%; Pred. No. 8.1e+04;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 9 IASLKQEIDALEY 21
Db 1 LBSLKKRVQLSF 13
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RESULT 18
Q4X244_ASPFU PRELIMINARY; PRT; 28 AA.
ID Q4X244
AC Q4X244
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afu2g07740;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AF293;
RA Niernman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman N., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kunagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penvalva M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Ruter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000001; EAL93071.1; -; Genomic_DNA.
SQ SEQUENCE 28 AA; 3148 MW; EED31A7594D35F59 CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 26.7%; Pred. No. 1.1e+05;
Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 9 IASLKQEDALEYEN 23
Db 3 ILLKSQLTLDFDS 17

RESULT 19
Q4XER1_PLACH PRELIMINARY; PRT; 28 AA.
ID Q4XER1
AC Q4XER1
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC042453.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAI01007241; CAI05471.1; -; Genomic_DNA.
SQ SEQUENCE 28 AA; 3629 MW; OCDB27595925A4B0 CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIAALKKQIASLKOE 15
Db 5 QIKQKKQKTQMKKK 19

RESULT 21
O62731_CANFA PRELIMINARY; PRT; 48 AA.
ID O62731_CANFA
AC O62731
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tropomyosin (Fragment).
GN Name=TPM1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.

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OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu P.-C., Chen Y.-W., Grob S.E., Katz M.L., Johnson G.S.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049587; AAC05499.1; -; Genomic DNA.
DR Ensembl; ENSCARG0000016966; Canis familiaris.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3251 MW; 5694A77F1CA73D30 CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 1.1e+05;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 KQKIASLKQEI 16
DB 12 ESKCAELEEL 22

RESULT 22
Q80KK2_9RHAB
ID Q80KK2_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KK2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paz A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192412; AAO31967.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2996 MW; 2F7337A9AACAC3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
DB 12 IDPISEAD 20

RESULT 23
Q80KLI_9RHAB
ID Q80KLI_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KLI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paz A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192403; AAO31958.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2938 MW; 2F7335C43ACA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
DB 12 IDPISEAD 20

RESULT 24
Q80KLI_9RHAB
ID Q80KLI_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KLI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paz A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192400; AAO31955.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2966 MW; 2F7335C425DA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
DB 12 IDPISEAD 20

RESULT 25
Q6DQP6_9RHAB
ID Q6DQP6_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q6DQP6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Polymerase (Fragment).
GN Name=L;
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C44/97;
RA Paz A., Saad C., Nunez C., Boshell J.;
RT "Molecular epidemiology of rabies in northern Colombia 1994-2003:
evidence for human and fox rabies associated with dogs.";
RL Epidemiol. Infect. 133:529-536(2005).
DR EMBL; AY649926; AAT66976.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2938 MW; 2F7335C43ACA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 16 IDALEYEND 24
 Db 12 IDPIESEAD 20

RESULT 26

Q6DQ03_9RHAB PRELIMINARY; PRT; 28 AA.
 AC Q6DQ03_9RHAB PRELIMINARY; PRT; 28 AA.
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Polymerase (Fragment).
 GN Name=L; virus.
 OS Rabies virus.
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 OX NCBI_TaxID=11292;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C41/97;
 RA Paez A., Saad C., Nunez C., Boshell J.;
 RA "Molecular epidemiology of rabies in northern Colombia 1994-2003:
 RT evidence for human and fox rabies associated with dogs.";
 RL Epidemiol. Infect. 133:529-536(2005).
 DR EMBL; AY649919; AAT66989.1; -; Genomic_RNA.
 FT NON TER 28
 SQ SEQUENCE 28 AA; 2996 MW; 2F7337A9ACA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
 Best Local Similarity 55.6%; Pred. No. 1.1e+05;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
 Db 12 IDPIESEAD 20

RESULT 27

Q9NCS6_TRYCR PRELIMINARY; PRT; 28 AA.
 ID Q9NCS6_TRYCR PRELIMINARY; PRT; 28 AA.
 AC Q9NCS6_TRYCR PRELIMINARY; PRT; 28 AA.
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Tcpl7 protein (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
 OC Schizotrypanum.
 OX NCBI_TaxID=5693;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SO3;
 EX MEDLINE=20231759; PubMed=10767555; DOI=10.1016/S0378-1119(00)00074-3;
 RA Robello C., Gamarro F., Castanys S., Alvarez-Valin F.;
 RT "Evolutionary relationships in Trypanosoma cruzi: molecular
 RT phylogenetics supports the existence of a new major lineage of
 RT strains.";
 RL Gene 246:331-338(2000).
 DR EMBL; AF174410; AAF97719.1; -; Genomic_DNA.
 DR InterPro; IPR006175; Endoribon_LPSF.
 DR Pfam; PF01042; Ribonuc_L_PSP; 1.
 FT NON TER 1
 SQ SEQUENCE 28 AA; 2807 MW; 14910A845047712 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
 Best Local Similarity 80.0%; Pred. No. 1.4e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 ETDAL 19
 Db 19 EVDAL 23

RESULT 28

Q4X811_PLACH PRELIMINARY; PRT; 28 AA.
 ID Q4X811_PLACH PRELIMINARY; PRT; 28 AA.
 AC Q4X811_PLACH PRELIMINARY; PRT; 28 AA.
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC405179.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAJ01009035; CAH86965.1; -; Genomic_DNA.
 DR Hypothetical protein.
 KW SEQUENCE 28 AA; 3537 MW; 9F44F6D16F101DA CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 8 KIASLKQEIADALEYB 22
 Db 3 KIRKIFAEENNEINYE 17

RESULT 29

Q4YAC7_PLABE PRELIMINARY; PRT; 28 AA.
 ID Q4YAC7_PLABE PRELIMINARY; PRT; 28 AA.
 AC Q4YAC7_PLABE PRELIMINARY; PRT; 28 AA.
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB401815.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAJ01007122; CAI05297.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 28 AA; 3288 MW; 52CB801BB1CD1F21 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
 Best Local Similarity 41.7%; Pred. No. 1.4e+05;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 KIAALKQKIASL 12
|||:|:|:
Db 13 KITLIKHKRARI 24

RESULT 30

Q4YLX3 PLABE
ID Q4YLX3 PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YLX3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFName=PB400661.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karas M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC ENBL: CAAI01003759; CAAI0988.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3344 MW; FA2E795E21047FFE CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;

Best Local Similarity 57.1%; Pred. No. 1.4e+05;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 IASLKQE 15

:|:|:|

Db 22 LLSIKQE 28

RESULT 31

Q704W4_BOVIN
ID Q704W4_BOVIN PRELIMINARY; PRT; 28 AA.
AC Q704W4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Signal transducer and activator of transcription 3 (Fragment).
GN Name=stat3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Seyfert H.M., Wheeler T.T., Moolenaar A., Pitra C.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL ENBL: AJ520562; CAF06189.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR001217; STAT.
DR Pfam: PF02864; STAT_bind; 1.

FT NON TER 1

FT NON TER 28

SQ SEQUENCE 28 AA; 3242 MW; B6B8BCBFEF6D921 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;

Best Local Similarity 20.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 14 QEIDALEYENDALEQ 28

:|:|:|:|

Db 7 EELHLITFETEVHQ 21

RESULT 32

Q71KP5_SPIMX
ID Q71KP5_SPIMX PRELIMINARY; PRT; 28 AA.
AC Q71KP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribulose biphosphate carboxylase large subunit (Fragment).
GN Name=rbcL;
OS Spirogyra maxima.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Zygnemophyceae; Zygnematales;
OC Zygnemataceae; Spirogyra.
OX NCBI_TaxID=3180;
RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Lee J., Manhart J.R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR ENBL: AF482498; AAO05912.1; -; Genomic_DNA.

DR GO; GO:0009507; C:chloroplast; IEA.

DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .; IEA.

DR GO; GO:0016984; F:ribulose-biphosphate carboxylase activity; IEA.

DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.

DR InterPro: IPR000685; RuBisCO_large.

DR Pfam: PF00016; RuBisCO_large; 1.

KW Chloroplast.

FT NON TER 1

SQ SEQUENCE 28 AA; 3245 MW; 49986352677561A2 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;

Best Local Similarity 25.0%; Pred. No. 1.4e+05;

Matches 5; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20

:|:|:|:|

Db 7 ELAAACEVWKEIKFEFDID 26

RESULT 33

Q9RAV6_RENSA
ID Q9RAV6_RENSA PRELIMINARY; PRT; 28 AA.
AC Q9RAV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 22 kDa surface protein (Fragment).
OS Renibacterium salmoninarum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococineae; Micrococcaceae; Renibacterium.
OX NCBI_TaxID=1646;
RN [1]

RP PROTEIN SEQUENCE.

RL MEDLINE=95011493; PubMed=7926685; DOI=10.1016/0378-1097(94)90307-7;

RA Fredriksen A., Bakken V.;

RT "Identification of Renibacterium salmoninarum surface proteins by

RT radioiodination.";

RL FEMS Microbiol. Lett. 121:297-301(1994).

SQ SEQUENCE 28 AA; 3299 MW; BF84603AED21D2EF CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;

Best Local Similarity 21.1%; Pred. No. 1.4e+05; Mismatches 5; Indels 0; Gaps 0;	
Matches 4; Conservative	
QY	9 IASLKQEIADALEYENDAL 27
Db	4 VXXYXEAQVQNNYAXE 22
RESULT 34	
Q5F210 MOUSE	
ID	Q5F210_MOUSE PRELIMINARY; PRT; 28 AA.
AC	Q5F210; 2005 (TReMBLrel. 30, Created)
DT	10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT	10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE	Oxytelor binding protein 2 (Fragment).
GN	Names=Osbp2; ORFNames=RP23-309E11.7-004;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eumetazoa; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Dunn M.;
RL	Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AL731853; CAI51856.1; -; Genomic_DNA.
FT	NON_TER 28
SQ	SEQUENCE 28 AA; 3453 MW; 2BF5DACD2D68FCFC CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 57.1%; Pred. No. 1.4e+05;	
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	18 ALEYEND 24
Db	22 ALNVEQE 28
RESULT 35	
Q80KFI_9RHAB	
ID	Q80KFI_9RHAB PRELIMINARY; PRT; 28 AA.
AC	Q80KFI; 2003 (TReMBLrel. 24, Created)
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE	L protein (Fragment).
OS	Rabies virus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Lyssavirus.
OX	NCBI_TaxID=11292;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA	Paez A., Nunez C., Garcia C., Boshell J.;
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT	human and dog rabies associated with bats."
RL	J. Gen. Virol. 84:795-802(2003).
DR	EMBL; AY192391; AAO45866.1; -; Genomic_RNA.
FT	NON_TER 28
SQ	SEQUENCE 28 AA; 3153 MW; 2E3266A9AAD64C6A CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 44.4%; Pred. No. 1.4e+05;	
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY	16 IDALEYEND 24
Db	12 IDPIESEDE 20
RESULT 36	
Q80KG5_9RHAB	
ID	Q80KG5_9RHAB PRELIMINARY; PRT; 28 AA.
AC	Q80KG5; 2003 (TReMBLrel. 24, Created)
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE	L protein (Fragment).
OS	Rabies virus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Lyssavirus.
OX	NCBI_TaxID=11292;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA	Paez A., Nunez C., Garcia C., Boshell J.;
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT	human and dog rabies associated with bats."
RL	J. Gen. Virol. 84:795-802(2003).
DR	EMBL; AY192391; AAO45866.1; -; Genomic_RNA.
FT	NON_TER 28
SQ	SEQUENCE 28 AA; 3153 MW; 2E3266A9AAD64C6A CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 44.4%; Pred. No. 1.4e+05;	
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY	16 IDALEYEND 24
Db	12 IDPIESEDE 20
RESULT 37	
Q9PRN8_CARAU	
ID	Q9PRN8_CARAU PRELIMINARY; PRT; 28 AA.
AC	Q9PRN8; 2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE	GVTP-VASOACTIVE intestinal peptide.
OS	Carassius auratus (Goldfish).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Carassius.
OX	NCBI_TaxID=7957;
RN	[1]
RP	PROTEIN SEQUENCE.
RA	MEDLINE=96051491; PubMed=8536941; DOI=10.1006/gcen.1995.1113;
RA	Uesaka T., Yano K., Yamasaki M., Ando M.;
RT	"Somatostatin-, vasoactive intestinal peptide-, and granulin-like
RT	peptides isolated from intestinal extracts of goldfish, Carassius
RT	auratus."
RL	Gen. Comp. Endocrinol. 99:298-306(1995).
DR	HSSP; P18509; IGEA.
DR	GO; GO:0005576; C:extracellular region; IEA.
DR	GO; GO:0005179; F:hormone activity; IEA.
DR	InterPro; IPR000532; Glucagon.
DR	Pfam; PF00123; Hormone 2; 1.
DR	PRINTS; PR00275; GLUCAGON.
DR	SMART; SM00070; GLUCA; 1.
DR	PROSITE; PS00260; GLUCAGON; 1.
SQ	SEQUENCE 28 AA; 3278 MW; E706A67573FF6F2F CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 20.8%; Pred. No. 1.4e+05;	
Matches 5; Conservative 6; Mismatches 13; Indels 0; Gaps 0;	
QY	3 AALKQKIASLKQEIADALEYENDAL 26
Db	4 AVFTDYSRYEKQMAKKYLSVL 27
RESULT 38	
Q4RLC7_TETNG	
ID	Q4RLC7_TETNG PRELIMINARY; PRT; 28 AA.

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; Nature 431:946-957(2004).

RL [2]

RN NCLEOTIDE SEQUENCE.

RP Genoscope, Whitehead Institute Centre for Genome Research; RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

RL -1- CAUTION: The sequence shown here is derived from an CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is CC preliminary data.

CC EMBL; CAAE01014601; -; Genomic DNA.

DR EMBL; CAAE01014601; -; Genomic DNA.

SQ SEQUENCE 28 AA; 3111 MW; FB98EC78D4C0EECE CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 1.4e+05;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 13 KOBIDALEYENDAL 26
DB 8 EEIIQFLRTVSDAV 21
: : : : :
: : : : :

RESULT 40

Q4T3N5_TETNG PRELIMINARY; PRT; 28 AA.

AC Q4T3N5; 2005 (T-EMBLrel. 31, Created)

DT 13-SEP-2005 (T-EMBLrel. 31, Last sequenced update)

DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)

DE Chromosome undetermined SCAF9978, whole genome shotgun sequence. (Fragment).

DE ORFNames=GSTENG0007715001;

OS Tetraodon nigroviridis (Green puffer).

GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; OC Tetraodontidae; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=99883;

XP [1]

RN NCLEOTIDE SEQUENCE.

RP Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Authouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Rameau C., Skalli Z., Cattolico L., Poulin J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutancheau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype."; Nature 431:946-957(2004).

RL [2]

RN NCLEOTIDE SEQUENCE.

RP Genoscope, Whitehead Institute Centre for Genome Research; RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

RL -1- CAUTION: The sequence shown here is derived from an CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is CC preliminary data.

CC EMBL; CAAE01009978; CAF92497.1; -; Genomic DNA.

DR NON TER 1 1

FT NON TER 28 28

SQ SEQUENCE 28 AA; 3037 MW; 996E33BD98146314 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
Best Local Similarity 31.2%; Pred. No. 1.4e+05;

use as long as its content is in no way modified and this statement is not removed.

CC CC

CC CC

CC CC

DR EMBL: U68222; AA953104.1; -, mRNA.

DR InterPro: IPR000347; Metallthion_15p.

DR Pfam: PF01439; Metallothio_2; 1.

DR ProDom: PD001611; Metallthion_15p; 1.

KW Metal-binding; Metal-thiolate cluster.

FT NON TER 1

SQ SEQUENCE 28 AA; 2914 MW; 936F98ADB314F03A CRC64;

Query Match 15.9%; Score 21; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ENDA 25

Db 10 ENDA 13

RESULT 43

VI03_VACCP STANDARD; PRT; 28 AA.

AC Q00334;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Protein I3 (Fragment).

GN ORFNames=I3L;

OS Vaccinia virus (strain L-IVP) (VACV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=31531;

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RF MEDLINE=91066899; PubMed=2250685;

RA Riazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,

RA Mikriukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,

RA Malugin E.G.

RT "Molecular-biological study of vaccinia virus genome. II. Localization

RT and nucleotide sequence of vaccinia virus genes coding for proteins

RT 36K and 12K."

RL Mol. Biol. (Mosk.) 24:968-976(1990).

CC -I- MISCELLANEOUS: This protein is synthesized in the early as well as

CC the late phase of infection.

CC -I- SIMILARITY: Belongs to the poxviruses I3 family.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL: X61165; CAA43473.1; -, Genomic_DNA.

DR InterPro: IPR006754; Pox_I3_1_ssdna_bd.

DR Pfam: PF04661; Pox_I3_1

KW Early protein; Late protein.

FT NON TER 1

SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 15.9%; Score 21; DB 1; Length 28;

Best Local Similarity 50.0%; Pred. No. 1.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 20 EYENDA 25

Db 14 EYEDS 19

RESULT 44

VIP_CANFA STANDARD; PRT; 28 AA.

ID VIP CANFA

AC P63289; P04565;

5 LKQKIASLKQETDALE 20

3 LREAVALLTAQQTSL 18

SULT 41

Q4XPA5 PLACH PRELIMINARY; PRT; 28 AA.

Q4XPA5;

13-SEP-2005 (TrEMBLrel. 31, Created)

13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

Hypothetical protein.

ORFNames=PC108138.00.0;

Plasmodium chabaudi.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=5825;

[1]

NUCLEOTIDE SEQUENCE.

Hall N., Karias M., Raine J.D., Carlton J.M., Koolj T.W.A.,

Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

James K., Rutherford K., Harris B., Harris D., Churcher C.,

Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,

"A comprehensive survey of the Plasmodium life cycle by genomic,

transcriptomic, and proteomic analyses."

Science 307:82-86(2005).

-I- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

preliminary data.

EMBL: CAJ01004227; CAH81257.1; -, Genomic_DNA.

Hypothetical protein.

SEQUENCE 28 AA; 3205 MW; 0E80PBB396A347AC CRC64;

Query Match 16.3%; Score 21.5; DB 2; Length 28;

Best Local Similarity 42.9%; Pred. No. 1.6e+05;

Matches 6; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

1 KIAALKQKIASLKQ 14

15 KVLFIK-KLKSLKK 27

SULT 42

2_BRANA STANDARD; PRT; 28 AA.

Q96353;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

Metallothionein-like protein type 2 LSC210 (Fragment).

Name=LSC210;

Brassica napus (Rape).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

NCBI_TaxID=3708;

[1]

NUCLEOTIDE SEQUENCE.

STRAIN=cv. Falcon; TISSUE=Leaf;

Buchanan-Wollaston V., Ainsworth C.,

Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

-I- FUNCTION: Metallothioneins have a high content of cysteine

residues that bind various heavy metals.

-I- SIMILARITY: Belongs to the metallothionein superfamily. Type 15

family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

```
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vasoactive intestinal peptide (VIP) (Vasoactive intestinal
DE polypeptide).
GN Name=VIP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86313167; PubMed=3748846; DOI=10.1016/0196-9781(86)90158-0;
RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
CC -!- FUNCTION: VIP causes vasodilation, lowers arterial blood pressure,
CC stimulates myocardial contractility, increases glycolysis and
CC relaxes the smooth muscle of trachea, stomach and gall bladder.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P18509; IGEA.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; Hormone 2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Amidation; Direct protein sequencing; Glucagon family; Hormone.
FT MOD_RES 28 28 Asparagine amide.
SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 15.9%; Score 21; DB 1; Length 28;
Best Local Similarity 20.8%; Pred. No. 1.8e+05;
Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKEIDALEYENDAL 26
Db |:::|
4 AVFTDNYTLRKQMAVKYLSIL 27

RESULT 45
ID VIP_CAPHI STANDARD; PRT; 28 AA.
AC P63290; P04565;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vasoactive intestinal peptide (VIP) (Vasoactive intestinal
DE polypeptide).
GN Name=VIP;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86313167; PubMed=3748846; DOI=10.1016/0196-9781(86)90158-0;
RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
```

```
CC -!- FUNCTION: VIP causes vasodilation, lowers arterial blood pressure,
CC stimulates myocardial contractility, increases glycolysis and
CC relaxes the smooth muscle of trachea, stomach and gall bladder.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P18509; IGEA.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; Hormone 2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Amidation; Direct protein sequencing; Glucagon family; Hormone.
FT MOD_RES 28 28 Asparagine amide.
SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 15.9%; Score 21; DB 1; Length 28;
Best Local Similarity 20.8%; Pred. No. 1.8e+05;
Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKEIDALEYENDAL 26
Db |:::|
4 AVFTDNYTLRKQMAVKYLSIL 27

Search completed: November 21, 2005, 21:46:22
Job time : 144 secs
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Query Match          34.8%; Score 46; DB 1; Length 28;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 8; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQEIDALE 20
   |:|:::|:|:::|
Db 4 KKLAKLEKALKEKALE 23

RESULT 2
PCT-US92-06412-1
; Sequence 1, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 4) 4"
PCT-US92-06412-1

Query Match          34.8%; Score 46; DB 4; Length 28;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 8; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQEIDALE 20
   |:|:::|:|:::|
Db 4 KKLAKLEKALKEKALE 23

RESULT 3
US-08-182-175A-3
; Sequence 3, Application US/08182175A
; Patent No. 5559223
```

```
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7) 4"
US-08-182-175A-3

Query Match          30.3%; Score 40; DB 1; Length 28;
Best Local Similarity 25.0%; Pred. No. 42;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQEIDALE 20
   |:|:::|:|:::|
Db 4 KKLAKLEKALKEKALE 23

RESULT 4
US-08-474-633A-70
; Sequence 70, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; APPLICANT: COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; TITLE OF INVENTION: METHODS FOR INCREASING
; TITLE OF INVENTION: INCREASING THE LYSINE
; TITLE OF INVENTION: AND THREONINE CONTENT
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
```

;; CITY: WILMINGTON
;; STATE: DELAWARE
;; COUNTRY: U.S.A.
;; ZIP: 19898
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; OPERATING SYSTEM: IBM PC COMPATIBLE
;; SOFTWARE: MICROSOFT WORD VERSION 2.0C
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/474,633A
;; FILING DATE:
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BARBARA C. SIEGELL
;; REGISTRATION NUMBER: 30,684
;; REFERENCE/DOCKET NUMBER: BB-1037-C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-4931
;; TELEFAX: 302-773-0164
;; TELEX: 835420
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..28
;; OTHER INFORMATION: /label= name
;; /note= "(SSP 7)4"
;; US-08-474-633A-70

Query Match 30.3%; Score 40; DB 1; Length 28;
Best Local Similarity 25.0%; Pred. No. 42;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQSIDALE 20
|:|::|:|::|:|
Db 4 KKLAMEEKLKAMEEKLKAME 23

RESULT 5
US-08-823-771-70
; Sequence 70, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/474,633
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BARBARA C. SIEGELL
;; REGISTRATION NUMBER: 30,684
;; REFERENCE/DOCKET NUMBER: BB-1037-C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-4931
;; TELEFAX: 302-773-0164
;; TELEX: 835420
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..28
;; OTHER INFORMATION: /label= name
;; /note= "(SSP 7)4"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
;; US-08-823-771-70

Query Match 30.3%; Score 40; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 42;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQSIDALE 20
|:|::|:|::|:|
Db 4 KKLAMEEKLKAMEEKLKAME 23

RESULT 6
PCT-US92-06412-3
; Sequence 3, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7) 4"
PCT-US92-06412-3

Query Match 30.3%; Score 40; DB 4; Length 28;

Best Local Similarity 25.0%; Pred. No. 42;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|:|:|:|:|:|:|
Db 4 KVKAMEEKVKAMEEKVKAME 23

RESULT 7

US-08-182-175A-2

; Sequence 2, Application US/08182175A

; Patent No. 5559223

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/182,175A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..28

; OTHER INFORMATION: /label= name

; OTHER INFORMATION: /note= "(SSP 5) 4"

US-08-182-175A-2

Query Match

28.0%; Score 37; DB 1; Length 28;

Best Local Similarity 25.0%; Pred. No. 11e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|:|:|:|:|:|:|
Db 4 KVKAMEEKVKAMEEKVKAME 23

RESULT 8

US-08-182-175A-39

; Sequence 39, Application US/08182175A

; Patent No. 5559223

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/182,175A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Linda Axamethy Floyd

; REGISTRATION NUMBER: 33,692

; REFERENCE/DOCKET NUMBER: BB-1031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 992-4929

; TELEFAX: (302) 892-7949

; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-182-175A-39

Query Match 28.0%; Score 37; DB 1; Length 28;

Best Local Similarity 25.0%; Pred. No. 11e+02;

Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|:~::~|:|
Db 4 KVKAMEEKVKAMEEKVKAME 23

RESULT 9

US-08-182-175A-43

; Sequence 43, Application US/08182175A

; Patent No. 5559223

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco

; APPLICANT: Sharon J. Keeler

; APPLICANT: Janet A. Rice

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:


```
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 5)4"
; US-08-474-633A-67

Query Match 28.0%; Score 37; DB 1; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLQKQIDALE 20
Db 4 KMKAMEEKMKAMEEKMAE 23

RESULT 15
US-08-944-133-18
; Sequence 18, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Rannels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE:
; APPLICATION NUMBER: US/08/232,525
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rannels, John H
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 504 387-3221
; TELEFAX: 504 346-8049
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-944-133-31

Query Match 28.0%; Score 37; DB 1; Length 28;
Best Local Similarity 36.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 4 ALKQKIASLQKQIDALEYENDALEQ 28
Db 2 ALKALKALKKALKKALKKALKK 26

RESULT 17
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-944-133-18

Query Match 28.0%; Score 37; DB 1; Length 28;
Best Local Similarity 34.6%; Pred. No. 1.1e+02;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 IAALKQKIASLQKQIDALEYENDALE 27
Db 3 LKALKKALKKALKKALKKALKKALK 28

RESULT 16
US-08-944-133-31
; Sequence 31, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Rannels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE:
; APPLICATION NUMBER: US/08/232,525
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rannels, John H
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 504 387-3221
; TELEFAX: 504 346-8049
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-944-133-31

Query Match 28.0%; Score 37; DB 1; Length 28;
Best Local Similarity 36.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 4 ALKQKIASLQKQIDALEYENDALEQ 28
Db 2 ALKALKALKKALKKALKKALKK 26

RESULT 17
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Query Match	Best Local Similarity	Score	DB 2;	Length	28;	Indels	Gaps	0;
US-09-320-424-16	US-09-320-424-16	28.0%;	Score 37;	DB 2;	Length 28;	0;	0;	0;
Sequence 16, Application US/09320424	Sequence 16, Application US/09320424	50.0%;	Pred. No. 1.1e+02;			0;	0;	0;
Patent No. 6284236	Patent No. 6284236	6;	Mismatches	0;	Indels	0;	Gaps	0;
GENERAL INFORMATION:	GENERAL INFORMATION:							
APPLICANT: Wiley, Steven R.	APPLICANT: Goodwin, Raymond G.							
TITLE OF INVENTION: Cycokine that Induces Apoptosis	TITLE OF INVENTION: Cycokine that Induces Apoptosis							
FILE REFERENCE: 2835-E	FILE REFERENCE: 2835-E							
CURRENT APPLICATION NUMBER: US/09/320,424	CURRENT APPLICATION NUMBER: US/09/320,424							
EARLIER FILING DATE: 1999-05-26	EARLIER FILING DATE: 1999-05-26							
EARLIER APPLICATION NUMBER: 09/190,046	EARLIER APPLICATION NUMBER: 09/190,046							
EARLIER FILING DATE: 1998-11-10	EARLIER FILING DATE: 1998-11-10							
EARLIER APPLICATION NUMBER: 09/048,641	EARLIER APPLICATION NUMBER: 09/048,641							
EARLIER FILING DATE: 1998-03-26	EARLIER FILING DATE: 1998-03-26							
EARLIER APPLICATION NUMBER: 08/670,354	EARLIER APPLICATION NUMBER: 08/670,354							
EARLIER FILING DATE: 1996-06-25	EARLIER FILING DATE: 1996-06-25							
EARLIER APPLICATION NUMBER: 08/548,368	EARLIER APPLICATION NUMBER: 08/548,368							
EARLIER FILING DATE: 1995-11-01	EARLIER FILING DATE: 1995-11-01							
EARLIER APPLICATION NUMBER: 08/496,632	EARLIER APPLICATION NUMBER: 08/496,632							
EARLIER FILING DATE: 1995-06-29	EARLIER FILING DATE: 1995-06-29							
NUMBER OF SEQ ID NOS: 25	NUMBER OF SEQ ID NOS: 25							
SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: PatentIn Ver. 2.0							
SEQ ID NO 16	SEQ ID NO 16							
LENGTH: 28	LENGTH: 28							
TYPE: PRT	TYPE: PRT							
ORGANISM: LZ peptide	ORGANISM: LZ peptide							
US-09-320-424-16	US-09-320-424-16							
Query Match	Query Match	28.0%;	Score 37;	DB 2;	Length 28;	0;	0;	0;
Best Local Similarity	Best Local Similarity	50.0%;	Pred. No. 1.1e+02;			0;	0;	0;
Matches	Matches	6;	Conservative	6;	Mismatches	0;	Indels	0;
QY	QY	9	IASLKQEIDALE 20					
DB	DB	2	LASLROQLLEALQ 13					
RESULT 18	RESULT 18							
US-09-320-424-17	US-09-320-424-17							
Sequence 17, Application US/09320424	Sequence 17, Application US/09320424							
Patent No. 6284236	Patent No. 6284236							
GENERAL INFORMATION:	GENERAL INFORMATION:							
APPLICANT: Wiley, Steven R.	APPLICANT: Goodwin, Raymond G.							
TITLE OF INVENTION: Cycokine that Induces Apoptosis	TITLE OF INVENTION: Cycokine that Induces Apoptosis							
FILE REFERENCE: 2835-E	FILE REFERENCE: 2835-E							
CURRENT APPLICATION NUMBER: US/09/320,424	CURRENT APPLICATION NUMBER: US/09/320,424							
EARLIER FILING DATE: 1999-05-26	EARLIER FILING DATE: 1999-05-26							
EARLIER APPLICATION NUMBER: 09/190,046	EARLIER APPLICATION NUMBER: 09/190,046							
EARLIER FILING DATE: 1998-11-10	EARLIER FILING DATE: 1998-11-10							
EARLIER APPLICATION NUMBER: 09/048,641	EARLIER APPLICATION NUMBER: 09/048,641							
EARLIER FILING DATE: 1998-03-26	EARLIER FILING DATE: 1998-03-26							
EARLIER APPLICATION NUMBER: 08/670,354	EARLIER APPLICATION NUMBER: 08/670,354							
EARLIER FILING DATE: 1996-06-25	EARLIER FILING DATE: 1996-06-25							
EARLIER APPLICATION NUMBER: 08/548,368	EARLIER APPLICATION NUMBER: 08/548,368							
EARLIER FILING DATE: 1995-11-01	EARLIER FILING DATE: 1995-11-01							
EARLIER APPLICATION NUMBER: 08/496,632	EARLIER APPLICATION NUMBER: 08/496,632							
EARLIER FILING DATE: 1995-06-29	EARLIER FILING DATE: 1995-06-29							
NUMBER OF SEQ ID NOS: 25	NUMBER OF SEQ ID NOS: 25							
SOFTWARE: PatentIn Ver. 2.0	SOFTWARE: PatentIn Ver. 2.0							
SEQ ID NO 17	SEQ ID NO 17							
LENGTH: 28	LENGTH: 28							
TYPE: PRT	TYPE: PRT							
ORGANISM: LZ peptide	ORGANISM: LZ peptide							

ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-08-823-771-40
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
Qy 1 KIAALKOKIASLKOEIDALE 20
|:|::|:|:|:|:|:|:
Db 4 KKKAWEKKKAMEKKKAME 23
RESULT 21
US-08-823-771-56
; Sequence 56, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; METHODS FOR INCREASING
; INCREASING THE LYSINE
; AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 835420
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-08-823-771-56
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
Qy 1 KIAALKOKIASLKOEIDALE 20
|:|:|:|:|:|:|:|:
Db 4 KKKAWEKKKAMEKKKAME 23
RESULT 22
US-08-823-771-67
; Sequence 67, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; METHODS FOR INCREASING
; INCREASING THE LYSINE
; AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 835420
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 5)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-08-823-771-67

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKKQIASLKQEIDALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 23
US-09-825-563-16
; Sequence 16, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; TYPE: PRT
; LENGTH: 28
; ORGANISM: LZ peptide
US-09-825-563-16

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IASLKQEIDALE 20
Db 2 IASIRQQIEAIQ 13

RESULT 25
PCT-US92-06412-2
; Sequence 2, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
;
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;
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 5)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-08-823-771-67

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IASLKQEIDALE 20
Db 2 IASIRQQIEAIQ 13

RESULT 25
PCT-US92-06412-2
; Sequence 2, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
;
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; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 5)4"
PCT-US92-06412-2

Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKOEIDALE 20
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 26
PCT-US92-06412-39
; Sequence 39, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; ZIP: 19898
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-39

Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKOEIDALE 20
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 27
PCT-US92-06412-43
; Sequence 43, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
```

```
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; ZIP: 19898
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-43

Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKOEIDALE 20
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 28
PCT-US92-06412-47
; Sequence 47, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; ZIP: 19898
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-43

Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKOEIDALE 20
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 29
PCT-US92-06412-49
; Sequence 49, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; ZIP: 19898
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-49
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; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-47

Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQETDALE 20
Db 4 KMKAMEEKMKAMEEKAME 23

RESULT 29
US-08-944-133-35
; Sequence 35, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE:
; APPLICATION NUMBER: US/08/232,525
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
; TELEPHONE: 504 387-3221
; TELEFAX: 504 346-8049
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-944-133-35
Query Match 27.3%; Score 36; DB 1; Length 28;
Best Local Similarity 36.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 IAALKQKIASLKQETDALEYNDAL 26
Db 4 LKALKKALKALKKALKALKAL 28

RESULT 30
US-09-082-279B-19
; Sequence 19, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-19

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 8 KIAALKQKIASLKQETDALE 27
Db 10 KVKLIKQELD--KYKNVTE 27

RESULT 31
US-09-082-279B-20
; Sequence 20, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-20

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;
```

Qy 8 KIASLKOEIDALEYENDALE 27
|: :|||:| :||| |
Db 3 KVKLIKQELD--KYKNAVTE 20

RESULT 32

US-09-082-279B-21
; Sequence 21, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-21

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KIASLKOEIDALEYENDALE 27
|: :|||:| :||| |
Db 7 KVKLIKQELD--KYKNAVTE 24

RESULT 33

US-08-474-349A-225
; Sequence 225, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-024
; CURRENT APPLICATION DATA:
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-226

; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-225

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KIASLKOEIDALEYENDALE 27
|: :|||:| :||| |
Db 10 KVKLIKQELD--KYKNAVTE 27

RESULT 34

US-08-474-349A-226
; Sequence 226, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-024
; CURRENT APPLICATION DATA:
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-226

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Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
Db      3 KVKLIKQELD--KYKNAVTE 20

RESULT 35
US-08-474-349A-227
; Sequence 227, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-227

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
Db      7 KVKLIKQELD--KYKNAVTE 24

RESULT 36
US-09-315-304B-19
; Sequence 19, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-19

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
Db      3 KVKLIKQELD--KYKNAVTE 20

RESULT 37
US-09-315-304B-20
; Sequence 20, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-20

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
Db      3 KVKLIKQELD--KYKNAVTE 20

RESULT 38
US-09-315-304B-21
; Sequence 21, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
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; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
;
US-09-515-965A-19

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 27

RESULT 43
US-09-515-965A-20
; Sequence 20, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
;
US-09-515-965A-20

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 27

RESULT 44
US-09-515-965A-21
; Sequence 21, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
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; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
;
US-09-515-965A-21

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 24

RESULT 45
US-09-350-641C-19
; Sequence 19, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
;
US-09-350-641C-19

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 27

Search completed: November 21, 2005, 21:41:31
Job time : 31.5 secs
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:41:39 ; Search time 106.5 Seconds
(without alignments)
109.852 Million cell updates/sec

Title: US-10-088-417A-1

Perfect score: 132

Sequence: 1 KIAALKQKIASLKQEIDALEYENDALSEQ 28

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 5696

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	43.2	28	4	US-10-360-053-23
2	54	40.9	28	4	US-10-360-053-22
3	51	38.6	28	3	US-09-320-907B-6
4	51	38.6	28	4	US-10-447-232-6
5	45	34.1	28	4	US-10-360-053-21
6	40	30.3	28	4	US-10-023-066A-70
7	40	30.3	28	5	US-10-804-678-70
8	39	29.5	28	5	US-10-830-959-6
9	37	28.0	28	4	US-10-023-066A-36
10	37	28.0	28	4	US-10-023-066A-40
11	37	28.0	28	4	US-10-023-066A-56
12	37	28.0	28	4	US-10-023-066A-67
13	37	28.0	28	4	US-10-652-244-16
14	37	28.0	28	4	US-10-652-244-17
15	37	28.0	28	5	US-10-804-678-36
16	37	28.0	28	5	US-10-804-678-40
17	37	28.0	28	5	US-10-804-678-56
18	37	28.0	28	5	US-10-804-678-67
19	37	28.0	28	5	US-10-900-399-16
20	37	28.0	28	5	US-10-900-399-17
21	36	27.3	28	4	US-10-351-641-19
22	36	27.3	28	4	US-10-351-641-20
23	36	27.3	28	4	US-10-351-641-21
24	36	27.3	28	5	US-10-950-010-331
25	35	26.5	28	4	US-10-267-682-85
26	35	26.5	28	4	US-10-267-748-85
27	35	26.5	28	5	US-10-706-275-6

28	34	25.8	28	3	US-09-945-917-23	Sequence 23, Appl
29	33	25.0	28	4	US-10-023-066A-58	Sequence 58, Appl
30	33	25.0	28	5	US-10-804-678-58	Sequence 58, Appl
31	32	24.2	28	3	US-09-739-307-173	Sequence 173, Appl
32	32	24.2	28	3	US-09-945-917-24	Sequence 24, Appl
33	32	24.2	28	3	US-09-938-671-173	Sequence 173, Appl
34	32	24.2	28	4	US-10-080-608A-2	Sequence 2, Appl
35	32	24.2	28	4	US-10-370-685-91	Sequence 91, Appl
36	32	24.2	28	4	US-10-267-682-86	Sequence 86, Appl
37	32	24.2	28	4	US-10-267-748-86	Sequence 86, Appl
38	32	24.2	28	5	US-10-851-691-10	Sequence 10, Appl
39	32	24.2	28	5	US-10-935-098-173	Sequence 173, Appl
40	32	24.2	28	5	US-10-892-981A-10	Sequence 10, Appl
41	31	23.5	28	3	US-09-864-761-44899	Sequence 44899, A
42	30	22.7	28	3	US-09-864-761-42292	Sequence 42292, A
43	30	22.7	28	4	US-10-351-641-18	Sequence 18, Appl
44	30	22.7	28	5	US-10-862-195-1275	Sequence 1275, Ap
45	29.5	22.3	28	4	US-10-351-641-77	Sequence 77, Appl

ALIGNMENTS

RESULT 1
US-10-360-053-23
; Sequence 23, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-23

Query Match 43.2%; Score 57; DB 4; Length 28;
Best Local Similarity 60.0%; Pred. No. 4;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Oy 1 KIAALKQKIASLKQEIDALE 20
| | | | | : | | | | | : | |
Db 5 KQAAIKNEIAAIAKQETAAIE 24

RESULT 2
US-10-360-053-22
; Sequence 22, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376

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; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 22
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-22

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Query Match 40.9%; Score 54; DB 4; Length 28;
Best Local Similarity 55.0%; Pred. No. 4.9;
Matches 11; Conservative 6; Mismatches 3; Indels

Qy 1 KIAALKQKIASLKQEIDALE 20
|||||::|||:::| | |
Db 5 KIAAIEEKIAOIEEEIAAOE 24

```

RESULT 3
US-09-320-907B-6
; Sequence 6, Application US/09320907B
; Publication No. US20020198360A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PFAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/09/320,907B
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; US-09-320-907B-6

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Query Match      38.6%; Score 51; DB 3; Length 28;
Best Local Similarity 40.7%; Pred. No. 12;
Matches 11: Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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QY 1 KIAALKQKIASLKQEIDALEYENDALE 27
 | : || : : : : |||
Db 1 KLEALEGRIDALEGKLEALEGKLDALE 27

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RESULT 4
US-10-447-292-6
; Sequence 6, Application US/10447292
; Publication No. US20030224453A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PFAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOSOLIC
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/10/447,292
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/320,907B
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 28
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-447-292-6

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Query Match 38.6%; Score 51; DB 4; Length 28;
Best Local Similarity 40.7%; Pred. No. 12;
Matches 11; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALEYENDALE 27
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Pb 1 KLEALEGRIDALEGKLEALEGLDALE 27

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RESULT 5
US-10-360-053-21
; Sequence 21, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembling a
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: INX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-21

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Query Match 34.1%; Score 45; DB 4; Length 28;
Best Local Similarity 56.2%; Pred. No. 72;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEI 16
:|::|::|::|::|
Db 12 EIAAIKDKIAAIKEIYI 27

RESULT 6
US-10-023-066A-70
; Sequence 70, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE AND
; THREONINE CONTENT OF THE SEEDS OF
; PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-023-066A-70

Query Match 30.3%; Score 40; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQKIDALE 20
Db 4 KLKAMEEKLKAMEEKLKAME 23

RESULT 7
US-10-804-678-70
; Sequence 70, Application US/10804678
; Publication No. US20050005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE CONTENT OF
; THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
```

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; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-804-678-70

Query Match 30.3%; Score 40; DB 5; Length 28;
Best Local Similarity 25.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQKIDALE 20
Db 4 KLKAMEEKLKAMEEKLKAME 23

RESULT 8
US-10-830-959-6
; Sequence 6, Application US/10830959
; Publication No. US20040259201A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Howard
; APPLICANT: Nadesalingam, Palaniyar
; APPLICANT: Reid, Kenneth
; APPLICANT: Strong, Peter
; TITLE OF INVENTION: Recombinant Surfactant Protein D Compositions and Methods of Use
; FILE REFERENCE: 18396/2402
; CURRENT APPLICATION NUMBER: US/10/830,959
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: PCT/GB02/04824
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: GB 0125638.7
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: GB 0209619.6
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-830-959-6

Query Match 29.5%; Score 39; DB 5; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IASLKQKIDALE 20
Db 2 VASLRQQVEALQ 13

RESULT 9
US-10-023-066A-36
; Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
```

```
/
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|::|:|
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 10
US-10-023-066A-40
; Sequence 40, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|::|:|
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 10
US-10-023-066A-40
; Sequence 40, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
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/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-023-066A-40
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|::|:|
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 11
US-10-023-066A-56
; Sequence 56, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-023-066A-56
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
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US-10-652-244-17

```

Query Match      28.0%; Score 37; DB 4; Length 20;
Best Local Similarity 50.0%; Pred.No. 7.8e+02;
Matches 6; Conservative 6; Mismatches 0; Indels

Qy 9 IASLKQIEDALE 20
    | | | | | | | | | |
Db 2 IASIROOIEAIO 13

```

RESULT 15

US-10-804-678-36
; Sequence 36, Application US/10804678
; Publication No. US2005005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE CONTENT OF
; THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.

Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels

RESULT 16

US-10-804-678-40
; Sequence 40, Application US/10804678

```

> Publication No. US2005005330A1
>
> GENERAL INFORMATION:
> APPLICANT: EPELBAUM, SABINE URSULA
>             FALCO, SAVERIO CARL
>             MCDEVITT, RAYMOND ERVIN, III
> TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
>             INCREASING THE LYSINE CONTENT OF
>             THE SEEDS OF PLANTS
>
> NUMBER OF SEQUENCES: 132
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
> STREET: 1007 MARKET STREET
> CITY: WILMINGTON
> STATE: DELAWARE
> COUNTRY: U.S.A.
> ZIP: 19898
>
> COMPUTER READABLE FORM:
> MEDIUM TYPE: DISKETTE, 3.50 INCH
> COMPUTER: IBM PC COMPATIBLE
> OPERATING SYSTEM: MICROSOFT OFFICE 97
> SOFTWARE: MICROSOFT WINDOWS 95
>
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/10/804,678
> FILING DATE: 19-Mar-2004
> CLASSIFICATION: <Unknown>
>
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US/09/049,304
> FILING DATE: 27-Mar-1998
> APPLICATION NUMBER: 08/824,627
> FILING DATE: MARCH 27, 1997
>
> ATTORNEY/AGENT INFORMATION:
> NAME: CHRISTENBURY, LYNN M.
> REGISTRATION NUMBER: 30,971
> REFERENCE/DOCKET NUMBER: BB-1037-F
>
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 302-992-5481
> TELEFAX: 302-892-7949
> TELEX: 835420
>
> INFORMATION FOR SEQ ID NO: 40:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 28 amino acids
> TYPE: amino acid
> TOPOLOGY: linear
>
> MOLECULE TYPE: protein
> SEQUENCE DESCRIPTION: SEQ ID NO: 40:
> US-10-804-678-40

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Query Match	28.0%	Score 37	DB 5	Length 28
Best Local Similarity	25.0%	Pred. No. 7.8e+02		
Matches	5	Conservative	12	Mismatches 3
				Indels 0
				Gaps 0

RESULT 17

US-10-804-678-56
; Sequence 56, Application US/10804678
; Publication No. US20050005330A1

US-10-804-678-40


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; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNN M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-804-678-56

Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIADALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 18
US-10-804-678-67
; Sequence 67, Application US/10804678
; Publication No. US20050005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE CONTENT OF
; THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998

```

```

; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNN M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 5)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-804-678-67

Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIADALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 19
US-10-900-399-16
; Sequence 16, Application US/10900399
; Publication No. US20050158823A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/900,399
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Lz peptide
US-10-900-399-16

Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IASLKQEIADALE 20
Db 1 IASLKQEIADALE 20

```

Db 2 IASLRQQLAQLQ 13

```
RESULT 20
US-10-900-399-17
; Sequence 17, Application US/10900399
; Publication No. US20050158823A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/900,399
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-900-399-17
```

Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 9 IASLRQQLAQLQ 20
Db 2 IASLRQQLAQLQ 13

```
RESULT 21
US-10-351-641-19
; Sequence 19, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Core polypeptide
US-10-351-641-19

Query Match 27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 8 KIASKQEIADALEYENDALE 27
Db 10 KVKLIQKQELD--KYKNAVTE 27

```
RESULT 22
US-10-351-641-20
; Sequence 20, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-20
```

Query Match 27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 8 KIASKQEIADALEYENDALE 27
Db 3 KVKLIQKQELD--KYKNAVTE 20

```
RESULT 23
US-10-351-641-21
; Sequence 21, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
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[illegible]

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-748-85

Query Match 26.5%; Score 35; DB 4; Length 28;
Best Local Similarity 47.1%; Pred. No. 1.4e+03;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 11 SLKQEIADLEYENDALE 27
DB 3 TLQAEIDQLEDEKSAIQ 19

RESULT 27
US-10-706-275-6
Sequence 6, Application US/10706275
Publication No. US20050002956A1
GENERAL INFORMATION:
APPLICANT: ID Biomedical Corporation of Quebec
APPLICANT: The Council of the Queensland Institute of Medical Research
APPLICANT: Lowell, George H.
APPLICANT: Burt, David S.
APPLICANT: White, Gregory L.
APPLICANT: Good, Michael F.
APPLICANT: Batzloff, Michael R.
APPLICANT: Leanderson, Tomas B.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: 021989-000710US
CURRENT APPLICATION NUMBER: US/10/706,275
CURRENT FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: AU 2002302132
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-6

Query Match 26.5%; Score 35; DB 5; Length 28;
Best Local Similarity 26.1%; Pred. No. 1.4e+03;

Matches 6; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 5 LKQKTASLKQEIADLEYENDALE 27
DB 2 LEDKVKQLRRDILDASREAKEBELQ 24

RESULT 28
US-09-945-917-23
Sequence 23, Application US/09945917
Publication No. US20030042381A1
GENERAL INFORMATION:
APPLICANT: Bogaert, Thierry
APPLICANT: Vandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REFERENCE: P/14-1
CURRENT APPLICATION NUMBER: US/09/945,917
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 28
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-945-917-23

Query Match 25.8%; Score 34; DB 3; Length 28;
Best Local Similarity 36.8%; Pred. No. 1.9e+03;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 IAALKQKIASLKQEIADALE 20
DB 5 LSTYKQKQLRQLKKDQKKLE 23

RESULT 29
US-10-023-066A-58
Sequence 58, Application US/10023066A
Publication No. US20030056242A1
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE AND
THREONINE CONTENT OF THE SEEDS OF
PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931


```
RESULT 33
US-09-938-671-173
; Sequence 173, Application US/09938671
; Publication No. US2004002066A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2022P1
; CURRENT APPLICATION NUMBER: US/09/938,671
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/348,457
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/070,567
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,692
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,704
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: 60/070,658
; PRIOR FILING DATE: 1998-01-07
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-671-173

Query Match      24.2%; Score 32; DB 3; Length 28;
Best Local Similarity 35.7%; Pred. No. 3.4e+03;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      6 KQKIASLKQKQIDAL 19
Db      13 EQKIEDISNKVDAM 26
      :|||: :|||:
      :|||: :|||:

RESULT 34
US-10-080-608A-2
; Sequence 2, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Probable variant of homo sapiens protein.
US-10-080-608A-2

Query Match      24.2%; Score 32; DB 4; Length 28;
Best Local Similarity 47.1%; Pred. No. 3.4e+03;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      11 SLKQEIDALEYENDALE 27
Db      3 TLQAEIDQLEDEKVALQ 19
      :|:|:|:|:|:|:|:|:|:
      :|:|:|:|:|:|:|:|:|:

RESULT 35
US-10-370-685-91
; Sequence 91, Application US/10370685
; Publication No. US20030215903A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 28
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: leucine zipper sequence
US-10-370-685-91

Query Match      24.2%; Score 32; DB 4; Length 28;
Best Local Similarity 47.1%; Pred. No. 3.4e+03;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      11 SLKQEIDALEYENDALE 27
Db      3 TLQAEIDQLEDEKVALQ 19
      :|:|:|:|:|:|:|:|:|:
      :|:|:|:|:|:|:|:|:|:

RESULT 36
US-10-267-682-86
; Sequence 86, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,283A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-267-682-86

Query Match 24.2%; Score 32; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAALKOKIASLKQE 15
DB 1 IARLEEKVKTLKAQ 14

RESULT 37
US-10-267-748-86
Sequence 86, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 863-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-267-748-86

Query Match 24.2%; Score 32; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAALKOKIASLKQE 15
DB 1 IARLEEKVKTLKAQ 14

RESULT 38
US-10-851-691-10
Sequence 10, Application US/10851691
Publication No. US20050009988A1
GENERAL INFORMATION:
APPLICANT: HARRIS, J. MILTON
APPLICANT: KOZLOWSKI, ANTONI
APPLICANT: MCMAHUS, SAMUEL P.
APPLICANT: BENTLEY, MICHAEL D.
APPLICANT: CHARLES, STEPHEN A.
TITLE OF INVENTION: POLYMER DERIVATIVES HAVING PARTICULAR ATOM ARRANGEMENTS
FILE REFERENCE: SHE0071.00
CURRENT APPLICATION NUMBER: US/10/851,691
CURRENT FILING DATE: 2004-05-21
PRIOR APPLICATION NUMBER: 60/493,213
PRIOR FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
US-10-851-691-10

Query Match 24.2%; Score 32; DB 5; Length 28;
Best Local Similarity 27.3%; Pred. No. 3.4e+03;
Matches 6; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 3 AALKOKIASLKQEIDALEYEND 24
DB 4 AVTENYTKLRKQLAAKKYLND 25

RESULT 39
US-10-935-098-173
Sequence 173, Application US/10935098
Publication No. US20050042667A1
GENERAL INFORMATION:
APPLICANT: Lafleur et al.
FILE REFERENCE: P2022P1C3
CURRENT APPLICATION NUMBER: US/10/935,098
CURRENT FILING DATE: 2004-09-08
PRIOR APPLICATION NUMBER: 09/938,671
PRIOR FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/739,907
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/348,457
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: PCT/US99/00108
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/070,657
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,704
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 173
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens

US-10-935-098-173

Query Match 24.2%; Score 32; DB 5; Length 28;
Best Local Similarity 35.7%; Pred. No. 3.4e+03;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 6 KQKIASLKQEIADL 19
Db 13 EQKIEDISNKVDAM 26
:||||: :|||:

RESULT 40

US-10-892-981A-10
; Sequence 10, Application US/10892981A
; Publication No. US20050043237A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Clark
; APPLICANT: Tutsuemi, Manami
; APPLICANT: Shanafelt, Armen B.
; TITLE OF INVENTION: Pituitary Adenylate Cyclase Activating Peptide (PACAP) Receptor 3
; TITLE OF INVENTION: (R3) Agonists an Their Pharmacological Methods of Use
; FILE REFERENCE: MSB 7272C1
; CURRENT APPLICATION NUMBER: US/10/892,981A
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 09/671,773
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/595,280
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/407,832
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 10
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(28)

US-10-892-981A-10

Query Match 24.2%; Score 32; DB 5; Length 28;
Best Local Similarity 27.3%; Pred. No. 3.4e+03;
Matches 6; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 3 AALKQKIASLKQEIADALEYEND 24
Db 4 AVPTENYTKURKQLAAKKYLND 25
| :|:::| :|||

RESULT 41

US-09-864-761-44899
; Sequence 44899, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44899
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121920.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
US-09-864-761-44899

Query Match 23.5%; Score 31; DB 3; Length 28;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 5 LKQKIASLKQEIADL 19
Db 11 LKAELTELADGL 25
|| :| :| :| :| :|

RESULT 42

US-09-864-761-42292
; Sequence 42292, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42292
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008392.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
US-09-864-761-42292
Query Match 22.7%; Score 30; DB 3; Length 28;
Best Local Similarity 31.6%; Pred. No. 6.2e+03;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 10 ASLKQEIIDALEVENDALEQ 28
Db 9 AOVQAEIEELQETQFALDK 27
RESULT 43
US-10-351-641-18
Sequence 18, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-18
Query Match 22.7%; Score 30; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 8 KIASLKQEIID 17
Db 17 KVKLIKQELD 26
RESULT 44
US-10-862-195-1275
Sequence 1275, Application US/10862195
Publication No. US20050164324A1
GENERAL INFORMATION:
APPLICANT: GYGI, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
FILE REFERENCE: 58890(70207)
CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,010
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1275
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments
OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1275
Query Match 22.7%; Score 30; DB 5; Length 28;
Best Local Similarity 53.8%; Pred. No. 6.2e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 15 EIDALEYENDALE 27
Db 4 ELDAYEAEGLALD 16
RESULT 45
US-10-351-641-77
Sequence 77, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09

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; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-77
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Query Match      22.3% Score 29.5; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.2e+03;
Matches 9; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
```

```
QY      10 ASLKQEIDAL-EYENDAL 26
      | | | | |
Db       5 AQLQTYDVLKDYNDAL 22
```

Search completed: November 21, 2005, 22:04:03
Job time : 107.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:46:35 ; Search time 4 seconds

(without alignments)
7.909 Million cell updates/sec

Title: US-10-088-417a-1

Perfect score: 132

Sequence: 1 KIALKQKIASLKQEDALEYENDALEQ 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 45

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /cgm2_6/ptodata/2/pubaa/US10_NEW_PUB pep.*
2: /cgm2_6/ptodata/2/pubaa/US06_NEW_PUB pep.*
3: /cgm2_6/ptodata/2/pubaa/US06_NEW_PUB pep.*
4: /cgm2_6/ptodata/2/pubaa/US08_NEW_PUB pep.*
5: /cgm2_6/ptodata/2/pubaa/US09_NEW_PUB pep.*
6: /cgm2_6/ptodata/2/pubaa/PCT_NEW_PUB pep.*
7: /cgm2_6/ptodata/2/pubaa/US11_NEW_PUB pep.*
8: /cgm2_6/ptodata/2/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	18.2	28	1	US-10-939-890-382
2	24	18.2	28	1	US-10-939-890-698
3	21	15.9	28	7	US-11-019-894A-21
4	19	14.4	28	1	US-10-939-890-325
5	19	14.4	28	1	US-10-939-890-346
6	19	14.4	28	1	US-10-939-890-355
7	19	14.4	28	1	US-10-939-890-383
8	19	14.4	28	1	US-10-939-890-899
9	19	14.4	28	1	US-10-939-890-822
10	19	14.4	28	1	US-10-939-890-831
11	18.5	14.0	28	1	US-10-939-890-385
12	18.5	14.0	28	1	US-10-939-890-701
13	18	13.6	28	1	US-10-997-201A-13
14	17	12.9	28	1	US-10-632-349-4
15	17	12.9	28	1	US-10-939-890-464
16	17	12.9	28	1	US-10-939-890-720
17	17	12.9	28	1	US-10-939-890-723
18	17	12.9	28	7	US-11-021-441-50
19	16	12.1	28	1	US-10-983-464-22
20	14	10.6	28	1	US-10-939-890-326
21	13	9.8	28	1	US-10-939-890-356
22	13	9.8	28	1	US-10-939-890-384
23	13	9.8	28	1	US-10-939-890-630
24	13	9.8	28	1	US-10-939-890-719
25	13	9.8	28	1	US-10-939-890-721

Sequence 722, App
Sequence 794, App
Sequence 795, App
Sequence 832, App
Sequence 847, App
Sequence 236, App
Sequence 344, App
Sequence 820, App
Sequence 353, App
Sequence 474, App
Sequence 726, App
Sequence 829, App
Sequence 351, App
Sequence 827, App
Sequence 3, Appli
Sequence 294, App
Sequence 10, Appl
Sequence 213, App
Sequence 345, App
Sequence 821, App

26 13 9.8 28 1 US-10-939-890-722
27 13 9.8 28 1 US-10-939-890-794
28 13 9.8 28 1 US-10-939-890-795
29 13 9.8 28 1 US-10-939-890-832
30 13 9.8 28 1 US-10-939-890-847
31 13 9.8 28 7 US-11-022-562-236
32 12.5 9.5 28 1 US-10-939-890-344
33 12.5 9.5 28 1 US-10-939-890-820
34 12 9.1 28 1 US-10-939-890-353
35 12 9.1 28 1 US-10-939-890-474
36 12 9.1 28 1 US-10-939-890-726
37 12 9.1 28 1 US-10-939-890-829
38 11 8.3 28 1 US-10-939-890-351
39 11 8.3 28 1 US-10-939-890-827
40 11 8.3 28 7 US-11-109-161-3
41 9 6.8 28 1 US-10-986-501-294
42 9 6.8 28 1 US-10-716-189-10
43 9 6.8 28 7 US-11-096-706-213
44 8 6.1 28 1 US-10-939-890-345
45 8 6.1 28 1 US-10-939-890-821

ALIGNMENTS

RESULT 1
US-10-939-890-382
; Sequence 382, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 382
LENGTH: 28
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-939-890-382

Query Match 18.2%; Score 24; DB 1; Length 28;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 19 LEYEND 24
 :|||
 Db 4 IEYVND 9

RESULT 2

US-10-939-890-698
 ; Sequence 698, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Bussat, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sudha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palaniappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle
 ; APPLICANT: Ramalingam, Kondareddiar
 ; APPLICANT: Shrivastava, Ajay
 ; APPLICANT: Song, Bo
 ; APPLICANT: Swenson, Rolf E.
 ; APPLICANT: Von Wronski, Mathew A.
 ; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 ; FILE REFERENCE: D0617.70014US09
 ; CURRENT APPLICATION NUMBER: US/10/939,890
 ; CURRENT FILING DATE: 2004-09-13
 ; PRIOR APPLICATION NUMBER: US 10/661,156
 ; PRIOR FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 10/382,082
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: PCT/US03/06731
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 883
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 698
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: ACETYLATION
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (28)..(28)
 ; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
 ; US-10-939-890-698

Query Match 18.2%; Score 24; DB 1; Length 28;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 19 LEYEND 24
 :|||
 Db 4 IEYVND 9

RESULT 3

US-11-019-894A-21
 ; Sequence 21, Application US/11019894A
 ; Publication No. US20050245451A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pincus, Matthew R.
 ; TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED
 ; FILE REFERENCE: 1181-17 CIP A
 ; CURRENT APPLICATION NUMBER: US/11/019,894A
 ; CURRENT FILING DATE: 2004-12-21
 ; PRIOR APPLICATION NUMBER: 10/386,737
 ; PRIOR FILING DATE: 2003-03-12
 ; PRIOR APPLICATION NUMBER: 09/827,683
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,102
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: 60/363,785
 ; PRIOR FILING DATE: 2002-03-12
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 21
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide; Human C-JUN membrane penetrating leader sequence
 ; US-11-019-894A-21

Query Match 15.9%; Score 21; DB 7; Length 28;
 Best Local Similarity 35.7%; Pred. No. 3.5e+02;
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQ 14
 :|||
 Db 12 RIAASKRRKKLER 25

RESULT 4

US-10-939-890-325
 ; Sequence 325, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Bussat, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sudha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palaniappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle
 ; APPLICANT: Ramalingam, Kondareddiar
 ; APPLICANT: Shrivastava, Ajay
 ; APPLICANT: Song, Bo
 ; APPLICANT: Swenson, Rolf E.
 ; APPLICANT: Von Wronski, Mathew A.
 ; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 ; FILE REFERENCE: D0617.70014US09
 ; CURRENT APPLICATION NUMBER: US/10/939,890
 ; CURRENT FILING DATE: 2004-09-13
 ; PRIOR APPLICATION NUMBER: US 10/661,156
 ; PRIOR FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 10/382,082
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: PCT/US03/06731
 ; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 883
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 325
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
 US-10-939-890-325

Query Match 14.4%; Score 19; DB 1; Length 28;
 Best Local Similarity 50.0%; Pred. No. 6.3e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 14 QEIDAL 19
 DB 16 QRVDSL 21

RESULT 5
 US-10-939-890-346
 ; Sequence 346, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Bussat, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sudha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palaniappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle
 ; APPLICANT: Ramalingam, Kondareddiar
 ; APPLICANT: Shrivastava, Ajay
 ; APPLICANT: Song, Bo
 ; APPLICANT: Swenson, Rolf E.
 ; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 ; FILE REFERENCE: D0617.70014US00
 ; CURRENT APPLICATION NUMBER: US/10/939,890
 ; CURRENT FILING DATE: 2004-09-13
 ; PRIOR APPLICATION NUMBER: US 10/661,156
 ; PRIOR FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 10/382,082
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: PCT/US03/06731
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 883
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 346

; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
 US-10-939-890-346

Query Match 14.4%; Score 19; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 DALE 20
 DB 3 DALE 6

RESULT 6

US-10-939-890-355
 ; Sequence 355, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Bussat, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sudha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palaniappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle
 ; APPLICANT: Ramalingam, Kondareddiar
 ; APPLICANT: Shrivastava, Ajay
 ; APPLICANT: Song, Bo
 ; APPLICANT: Swenson, Rolf E.
 ; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 ; FILE REFERENCE: D0617.70014US00

; CURRENT APPLICATION NUMBER: US/10/939,890
 ; CURRENT FILING DATE: 2004-09-13
 ; PRIOR APPLICATION NUMBER: US 10/661,156
 ; PRIOR FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 10/382,082
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: PCT/US03/06731
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 883
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 355

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
 US-10-939-890-355

Query Match 14.4%; Score 19; DB 1; Length 28;
 Best Local Similarity 33.3%; Pred. No. 6.3e+02;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 20 EYENDALEQ 28
 DB 2 QWESDYWDQ 10

RESULT 7

US-10-939-890-383
 ; Sequence 383, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.

; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 383
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-383

Query Match 14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 DALE 20
Db 3 DALE 6

RESULT 8
US-10-939-890-699
; Sequence 699, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)-(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-699

Query Match 14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 DALE 20
Db 3 DALE 6

RESULT 9
US-10-939-890-822
; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 883
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 822
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: ACETYLATION
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (9)..(9)
 ; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (28)..(28)
 ; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
 ; US-10-939-890-822

Query Match 14.4%; Score 19; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 DALE 20
 ||||
 Db 3 DALE 6

RESULT 10

; US-10-939-890-831
 ; Sequence 831, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Bussat, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sudha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palaniappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle
 ; APPLICANT: Ramalingam, Kondareddiar
 ; APPLICANT: Shrivastava, Ajay
 ; APPLICANT: Song, Bo
 ; APPLICANT: Swenson, Rolf E.
 ; APPLICANT: Von Wronski, Mathew A.
 ; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 ; FILE REFERENCE: D0617.70014US00
 ; CURRENT APPLICATION NUMBER: US/10/939,890
 ; CURRENT FILING DATE: 2004-09-13
 ; PRIOR APPLICATION NUMBER: US 10/661,156
 ; PRIOR FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 10/382,082
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: PCT/US03/06731
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 883
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 831
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: ACETYLATION
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (16)..(16)
 ; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (21)..(21)
 ; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (28)..(28)
 ; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
 ; US-10-939-890-831

Query Match 14.4%; Score 19; DB 1; Length 28;
 Best Local Similarity 33.3%; Pred. No. 6.3e+02;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 20 EYENDALEQ 28
 ::||:|:|
 Db 2 QWESDYWDQ 10

RESULT 11

; US-10-939-890-385
 ; Sequence 385, Application US/10939890
 ; Publication No. US20050250700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Aaron K.
 ; APPLICANT: Sexton, Daniel J.
 ; APPLICANT: Dransfield, Daniel T.
 ; APPLICANT: Ladner, Robert C.
 ; APPLICANT: Arbogast, Christophe
 ; APPLICANT: Bussat, Philippe
 ; APPLICANT: Fan, Hong
 ; APPLICANT: Khurana, Sudha
 ; APPLICANT: Linder, Karen E.
 ; APPLICANT: Marinelli, Edmund R.
 ; APPLICANT: Nanjappan, Palaniappa
 ; APPLICANT: Nunn, Adrian D.
 ; APPLICANT: Pillai, Radhakrishna
 ; APPLICANT: Pochon, Sibylle
 ; APPLICANT: Ramalingam, Kondareddiar
 ; APPLICANT: Shrivastava, Ajay
 ; APPLICANT: Song, Bo
 ; APPLICANT: Swenson, Rolf E.
 ; APPLICANT: Von Wronski, Mathew A.
 ; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 ; FILE REFERENCE: D0617.70014US00
 ; CURRENT APPLICATION NUMBER: US/10/939,890
 ; CURRENT FILING DATE: 2004-09-13
 ; PRIOR APPLICATION NUMBER: US 10/661,156
 ; PRIOR FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 10/382,082
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: PCT/US03/06731
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/440,411
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/360,851

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; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 385
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-385

Query Match      14.0%; Score 18.5; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 7.3e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY      13 KQRIDAL-EYENDA 25
       :||| | | | | | | |
Db      7 QERDKLREHYDDA 20

RESULT 12
US-10-939-890-701
; Sequence 701, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (26)..(28)

; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-701

Query Match      14.0%; Score 18.5; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 7.3e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY      13 KQRIDAL-EYENDA 25
       :||| | | | | | | |
Db      7 QERDKLREHYDDA 20

RESULT 13
US-10-997-201A-13
; Sequence 13, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-13

Query Match      13.6%; Score 18; DB 1; Length 28;
Best Local Similarity 60.0%; Pred. No. 8.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 QKIAS 11
       :|||
Db      11 EKVAS 15

RESULT 14
US-10-632-349-4
; Sequence 4, Application US/10632349
; Publication No. US20050250685A1
; GENERAL INFORMATION:
; APPLICANT: ZAVERI, CHANDA
; TITLE OF INVENTION: PEPTIDES WITH WOUND HEALING ACTIVITY
; FILE REFERENCE: 37896.00002.DIV3
; CURRENT APPLICATION NUMBER: US/10/632,349
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 09/879,666
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/211,859
; PRIOR FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Acetylation
US-10-632-349-4

Query Match      12.9%; Score 17; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      12 LKQEIDALE 20
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```
Db      ||::: :|
        16 LKKEKVEE 24

RESULT 15
US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-464

Query Match      12.9%; Score 17; DB 1; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      14 QEIDALEY 21
Db      ||::: :|
        6 QDMIRLDY 13

RESULT 16
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
```

```
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617 70014US09
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 893
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 723
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ NAME/KEY: MOD RES
/ LOCATION: (1)-(1)
/ OTHER INFORMATION: ACETYLATION
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (28)-(28)
/ OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-723

Query Match          12.9%; Score 17; DB 1; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      14 QETDALEY 21
Db      6 QDMIRLDY 13

RESULT 18
US-11-021-441-50
/ Sequence 50, Application US/11021441
/ Publication No. US20050249748A1
/ GENERAL INFORMATION:
/ APPLICANT: DUBENSKY, Thomas W., Jr.
/ APPLICANT: PORTNOY, Daniel A.
/ APPLICANT: LUCKETT, William S., Jr.
/ APPLICANT: COOK, David N.
/ TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
/ TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 282172003900
/ CURRENT APPLICATION NUMBER: US/11/021,441
/ CURRENT FILING DATE: 2004-12-23
/ PRIOR APPLICATION NUMBER: US 60/616,750
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/615,287
/ PRIOR FILING DATE: 2004-10-01
/ PRIOR APPLICATION NUMBER: US 60/599,377
/ PRIOR FILING DATE: 2004-08-05
/ PRIOR APPLICATION NUMBER: PCT/US2004/23881
/ PRIOR FILING DATE: 2004-07-23
/ PRIOR APPLICATION NUMBER: US 10/883,599
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: US 60/556,744
/ PRIOR FILING DATE: 2004-03-26
/ NUMBER OF SEQ ID NOS: 129

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 50
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Bacillus anthracis
US-11-021-441-50

Query Match          12.9%; Score 17; DB 7; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 KOKIAS 11
Db      3 KUKMAS 8

RESULT 19
US-10-983-464-22
/ Sequence 22, Application US/10983464
/ Publication No. US20050245446A1
/ GENERAL INFORMATION:
/ APPLICANT: Hailes, Helen C.
/ APPLICANT: Tabor, Alethea B.
/ APPLICANT: Wong, John B.
/ APPLICANT: Pilkington-Wiksa, Michael
/ APPLICANT: Hart, Stephen L.
/ APPLICANT: Hurley, Christopher A.
/ TITLE OF INVENTION: Materials For The Delivery of
/ TITLE OF INVENTION: Biologically-Active Material To Cells
/ FILE REFERENCE: 50318/008001
/ CURRENT APPLICATION NUMBER: US/10/983,464
/ CURRENT FILING DATE: 2004-11-08
/ PRIOR APPLICATION NUMBER: PCT/GB03/01985
/ PRIOR FILING DATE: 2003-05-08
/ PRIOR APPLICATION NUMBER: US 60/576,270
/ PRIOR FILING DATE: 2004-06-02
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 22
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-983-464-22

Query Match          12.1%; Score 16; DB 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      6 KOKIASLKOE 15
Db      13 KKKKGACRRE 22

RESULT 20
US-10-939-890-326
/ Sequence 326, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
```

Tue Nov 22 08:14:35 2005

APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 326
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-326

Query Match 10.6%; Score 14; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 QE1 16

Db 10 QE1 12

RESULT 21

US-10-939-890-356
Sequence 356, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-356

Query Match 9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 1.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 KIASLKQEI 16

Db 8 EILSMADQL 16

RESULT 22

US-10-939-890-384
Sequence 384, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 384
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-939-890-384

Query Match 9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 28.6%; Pred. No. 3.1e+03;

Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 20 EYNDAL 26
: : :
Db 2 QWYDGL 8

RESULT 23

US-10-939-890-630
; Sequence 630, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 630

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (1)..(1)

; OTHER INFORMATION: ACETYLATION

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (28)..(28)

; OTHER INFORMATION: Lys residue modified with a JJ spacer linker

US-10-939-890-630

Query Match 9.8%; Score 13; DB 1; Length 28;

Best Local Similarity 22.2%; Pred. No. 3.le+03;

Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 KIASKQEI 16

: : :
Db 8 EILSMADQL 16

RESULT 24

US-10-939-890-719

; Sequence 719, Application US/10939890

; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: Fast-SEQ for Windows Version 4.0

; SEQ ID NO 719

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (1)..(1)

; OTHER INFORMATION: ACETYLATION

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (28)..(28)

; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-719

Query Match 9.8%; Score 13; DB 1; Length 28;

Best Local Similarity 22.2%; Pred. No. 3.le+03;

Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 KIASKQEI 16

: : :
Db 8 EILSMADQL 16

RESULT 25

US-10-939-890-721

; Sequence 721, Application US/10939890

; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.

; APPLICANT: Sexton, Daniel J.

; APPLICANT: Dransfield, Daniel T.

; APPLICANT: Ladner, Robert C.

```

; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-01-15
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 721
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
US-10-939-890-721

```

```

Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      8 KIASLKQEI 16
      |||:
Db      8 EILSMADQL 16

```

```

RESULT 26
US-10-939-890-722
; Sequence 722, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.

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; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-01-15
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 722
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-722

```

```

Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      8 KIASLKQEI 16
      |||:
Db      8 EILSMADQL 16

```

```

RESULT 27
US-10-939-890-794
; Sequence 794, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

```

```
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 794
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (28)..(28)
/ OTHER INFORMATION: Lys residue modified with SATA linker
US-10-939-890-794
```

```
Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      8 KIASLKQEI 16
      |||||:
Db       8 EILSMADQL 16
```

```
RESULT 28
US-10-939-890-795
/ Sequence 795, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
```

```
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 795
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: ACETYLATION
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (28)..(28)
/ OTHER INFORMATION: Lys residue modified with SATA JJ spacer linker
US-10-939-890-795
```

```
Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      8 KIASLKQEI 16
      |||||:
Db       8 EILSMADQL 16
```

```
RESULT 29
US-10-939-890-832
/ Sequence 832, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 832
```

```

; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JV spacer linker
US-10-939-890-832

```

```

Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      8 KIASLKQEI 16
Db      8 EILSMADQL 16

```

RESULT 30

```

US-10-939-890-847
; Sequence 847, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 847
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)

```

```

; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a J spacer linker
US-10-939-890-847

```

```

Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      8 KIASLKQEI 16
Db      8 EILSMADQL 16

```

RESULT 31

```

US-11-022-562-236
; Sequence 236, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-236

```

```

Query Match          9.8%; Score 13; DB 7; Length 28;
Best Local Similarity 12.5%; Pred. No. 3.1e+03;
Matches 1; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      12 LKQEIDAL 19
Db      8 MPQDLNTM 15

```

RESULT 32

```

US-10-939-890-344
; Sequence 344, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

```

```

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-344
```

```

Query Match          9.5%; Score 12.5; DB 1; Length 28;
Best Local Similarity 44.4%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      13 KQRIDALEY 21
Db      3 KKE-DAQQW 10
```

```

RESULT 33
US-10-939-890-820
; Sequence 820, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```

; SEQ ID NO 820
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)..(4)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-820
```

```

Query Match          9.5%; Score 12.5; DB 1; Length 28;
Best Local Similarity 44.4%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      13 KQRIDALEY 21
Db      3 KKE-DAQQW 10
```

```

RESULT 34
US-10-939-890-353
; Sequence 353, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
```


FEATURE:
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-353

Query Match 9.1%; Score 12; DB 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 19 LEYENDALEQ 28
Db 12 LNYRPTMFHQ 21

RESULT 35
US-10-939-890-474
; Sequence 474, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-474

Query Match 9.1%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 14 QEIDAL 19
Db 14 QAEDSL 19

RESULT 36
US-10-939-890-726
; Sequence 726, Application US/10939890

Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 726
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-726

Query Match 9.1%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 14 QEIDAL 19
Db 14 QAEDSL 19

RESULT 37
US-10-939-890-829
; Sequence 829, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe

```

; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US 10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 829
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-829

```

```

Query Match          9.1%  Score 12;  DB 1;  Length 28;
Best Local Similarity 30.0%;  Pred. No. 3.8e+03;
Matches 3;  Conservative 0;  Mismatches 7;  Indels 0;  Gaps 0;

```

```

QY      19  LEYENDALEQ 28
Db       12  LNVKPTMFHQ 21

```

```

RESULT 38
US-10-939-890-351
; Sequence 351, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle

```

```

; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US 10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-351

```

```

Query Match          8.3%  Score 11;  DB 1;  Length 28;
Best Local Similarity 66.7%;  Pred. No. 4.5e+03;
Matches 2;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

QY      23  NDA 25
Db       17  DDA 19

```

```

RESULT 39
US-10-939-890-827
; Sequence 827, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US 10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411

```

;; PRIOR FILING DATE: 2003-01-15
;; PRIOR APPLICATION NUMBER: US 60/360,851
;; PRIOR FILING DATE: 2002-03-01
;; NUMBER OF SEQ ID NOS: 883
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 827
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
;; FEATURE:
;; NAME/KEY: MOD RES
;; LOCATION: (1)..(1)
;; OTHER INFORMATION: ACETYLATION
;; FEATURE:
;; NAME/KEY: MOD RES
;; LOCATION: (28)..(28)
;; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-827

Query Match 8.3%; Score 11; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 NDA 25
Db 17 DDA 19

RESULT 40
US-11-109-161-3
;; Sequence 3, Application US/1109161
;; Publication No. US2005024422A1
;; GENERAL INFORMATION:
;; APPLICANT: MASCARENHAS, Desmond
;; APPLICANT: SINGH, Baljit K.
;; TITLE OF INVENTION: METHODS FOR DELIVERING MED
;; TITLE OF INVENTION: PEPTIDE-LINKED AGENT INTO CELLS UNDER CONDITIONS OF CELLULAR
;; TITLE OF INVENTION: STRESS
;; FILE REFERENCE: 51490-20003.00
;; CURRENT APPLICATION NUMBER: US/11/109,161
;; CURRENT FILING DATE: 2005-04-18
;; PRIOR APPLICATION NUMBER: US 60/563,141
;; PRIOR FILING DATE: 2004-04-16
;; PRIOR APPLICATION NUMBER: US 60/563,676
;; PRIOR FILING DATE: 2004-04-19
;; PRIOR APPLICATION NUMBER: US 60/657,826
;; PRIOR FILING DATE: 2005-03-01
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic construct
US-11-109-161-3

Query Match 8.3%; Score 11; DB 7; Length 28;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KKK 8
Db 6 KKK 8

RESULT 41
US-10-986-501-294
;; Sequence 294, Application US/10986501
;; Publication No. US20050244845A1
;; GENERAL INFORMATION:

;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: 90 Human Secreted Proteins
;; FILE REFERENCE: P2013P2C1
;; CURRENT APPLICATION NUMBER: US/10/986,501
;; CURRENT FILING DATE: 2004-11-12
;; PRIOR APPLICATION NUMBER: US/10/621,363
;; PRIOR FILING DATE: 2003-07-18
;; PRIOR APPLICATION NUMBER: 09/969,730
;; PRIOR FILING DATE: 2001-10-06
;; PRIOR APPLICATION NUMBER: 09/774,639
;; PRIOR FILING DATE: 2001-02-01
;; PRIOR APPLICATION NUMBER: 60/238,291
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 09/244,112
;; PRIOR FILING DATE: 1999-02-04
;; PRIOR APPLICATION NUMBER: PCT/US98/16235
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/056,371
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: 60/056,732
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: 60/056,366
;; PRIOR FILING DATE: 1997-08-19
;; PRIOR APPLICATION NUMBER: 60/056,364
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 373
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 294
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-986-501-294

Query Match 6.8%; Score 9; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 5.8e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QKI 9
Db 10 QRL 12

RESULT 42
US-10-716-189-10
;; Sequence 10, Application US/10716189
;; Publication No. US20050249750A1
;; GENERAL INFORMATION:
;; APPLICANT: Nardin, Elizabeth
;; APPLICANT: Moreno, Alberto
;; TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
;; FILE REFERENCE: 5986/1B615-US1
;; CURRENT APPLICATION NUMBER: US/10/716,189
;; CURRENT FILING DATE: 2003-11-17
;; PRIOR APPLICATION NUMBER: US/09/060,450
;; PRIOR FILING DATE: 1998-01-21
;; PRIOR APPLICATION NUMBER: 60/033,916
;; PRIOR FILING DATE: 1997-01-21
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 10
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Fusion of Carboxyl Terminus of SEQ ID NO:4 to
;; OTHER INFORMATION: Amino Terminus of Seq ID NO: 1, designated T1B
US-10-716-189-10

Query Match 6.8%; Score 9; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.8e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      16 ID 17
Db      20 VD 21

RESULT 43
US-11-096-706-213
; Sequence 213, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-00822005
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (DNA binding domain)
US-11-096-706-213

Query Match      6.8%; Score 9; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      23 NDAL 26
Db      13 SDHL 16

RESULT 44
US-10-939-890-345
; Sequence 345, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION

Qy      19 LEY 21
Db      19 LFY 21

RESULT 45
US-10-939-890-821
; Sequence 821, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
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; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-821
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Query Match      6.1%; Score 8; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 6.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 19 LEY 21
   |||
Db 19 LFY 21
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Search completed: November 21, 2005, 22:04:16
Job time : 4.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:25:38; Search time 130 Seconds
(without alignments)
94.635 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWKNHLKQETAALEQBIAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 9880

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database: A_Geneseq_21.*
- 1: Geneseq1980s.*
 - 2: Geneseq1990s.*
 - 3: Geneseq2000s.*
 - 4: Geneseq2001s.*
 - 5: Geneseq2002s.*
 - 6: Geneseq2003as.*
 - 7: Geneseq2003bs.*
 - 8: Geneseq2004s.*
 - 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	100.0	28	AAB74346	Peptide S
2	137	100.0	28	AAB74347	Peptide S
3	124	90.5	28	AAB74349	Peptide S
4	123	89.8	28	AAB74348	Peptide S
5	123	89.8	28	AAB74356	Peptide u
6	123	89.8	28	AAB74352	Peptide S
7	122	89.1	28	AAB74345	Peptide S
8	105	76.6	28	ADM41438	Self-asse
9	81	59.1	28	ABR84737	DE novo d
10	75	54.7	28	AAB74343	Peptide S
11	75	54.7	28	AAB74351	Peptide S
12	75	54.7	28	ADM41436	Self-asse
13	74	54.0	28	AAB74341	Peptide S
14	74	54.0	28	AAB74342	Peptide S
15	70	51.1	28	AAB74355	Peptide u
16	70	51.1	28	AAB74350	Peptide S
17	59	43.1	28	ABR84735	DE novo d
18	54	39.4	28	ABR84736	DE novo d
19	45	32.8	28	AAU14021	Peptide s
20	45	32.8	28	ABO10240	Heptad re
21	45	32.8	28	ADB67071	Canonic
22	45	32.8	28	ADL99341	Nancostuc
23	44	32.1	28	AAR31979	SSP4 poly
24	42	30.7	28	ADY52134	Heparin b

25	41	29.9	28	9	ADY52132	Heparin b
26	39	28.5	28	4	AAB50879	Integrin
27	39	28.5	28	4	AAB59138	Alpha-hel
28	39	28.5	28	8	ADL15278	Prion pro
29	38	27.7	28	2	AAR31981	SSP7 poly
30	38	27.7	28	2	AAR78256	SSP(7)4 h
31	38	27.7	28	6	ADA15966	Synthetic
32	38	27.7	28	6	ABO44343	Ear I-bas
33	38	27.7	28	9	ADW71693	Peptide S
34	37	27.0	28	2	AAR34576	Domain 1
35	36	26.3	28	2	AAR32693	SSP poly
36	36	26.3	28	2	AAR32689	SSP poly
37	36	26.3	28	2	AAR31980	SSP(5)4 h
38	36	26.3	28	2	AAR78255	SSP 5.5.5
39	36	26.3	28	2	AAR78250	SSP 5.5.5
40	36	26.3	28	2	AAR78244	SSP 5.5.5
41	36	26.3	28	2	AAR78242	SSP 5.5.5
42	36	26.3	28	2	AAW62935	Minimilis
43	36	26.3	28	2	AAW60508	Synthetic
44	36	26.3	28	2	AAW60516	Synthetic
45	36	26.3	28	2	AAW60510	Synthetic

ALIGNMENTS

RESULT 1
AAB74346
ID AAB74346 standard; peptide; 28 AA.

XX AAB74346;
AC
XX
XX 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p2B.
XX
XX Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
XX WO200121646-A1.
XX
XX 29-MAR-2001.
PD
PF 18-SEP-2000; 2000WO-GB003576.
XX
XX 17-SEP-1999; 99GB-00022013.
PR
XX (UYSU-) UNIV SUSSEX.
PA
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
PI WPI; 2001-335468/35.
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 9; 45pp; English.

XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
XX present sequence is the peptide monomer unit SAF-p2B

SQ Sequence 28 AA;

Query Match 100.0%; Score 137; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIRALKWKNHLKQETAALEQBIAALEQ 28

```
Db      |||||||
1 KIRALKWNAHLKQETAALEQETAALEQ 28

RESULT 2
AAB74347
ID AAB74347 standard; peptide; 28 AA.
XX AC AAB74347;
XX DT 02-JUL-2001 (first entry)
XX DE Peptide SAF-p2C.
XX KW Atomic Force Microscopy; AFM.
XX OS Unidentified.
XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX DR WPI; 2001-335468/35.
XX CC New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2E
XX SQ Sequence 28 AA;

Query Match 90.5%; Score 124; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 28-09;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      |||||
1 KIRALKWNAHLKQETAALEQETAALEQ 28
Db      |||||
1 KIRALKWNAHLKQETAALEQETAALEQ 28

RESULT 4
AAB74348
ID AAB74348 standard; peptide; 28 AA.
XX AC AAB74348;
XX DT 02-JUL-2001 (first entry)
XX DE Peptide SAF-p2D.
XX KW Atomic Force Microscopy; AFM.
XX OS Unidentified.
XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX DR WPI; 2001-335468/35.
XX CC New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2D
XX SQ Sequence 28 AA;

Query Match 100.0%; Score 137; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      |||||||
1 KIRALKWNAHLKQETAALEQETAALEQ 28
Db      |||||||
1 KIRALKWNAHLKQETAALEQETAALEQ 28

RESULT 3
AAB74349
ID AAB74349 standard; peptide; 28 AA.
XX AC AAB74349;
XX DT 02-JUL-2001 (first entry)
XX DE Peptide SAF-p2E.
XX KW Atomic Force Microscopy; AFM.
XX OS Unidentified.
XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX DR WPI; 2001-335468/35.
XX CC New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2D
XX SQ Sequence 28 AA;
```



```
SQ Sequence 28 AA;

Query Match      89.8%; Score 123; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.7e-09;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIQAALQEQ 28
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 KIRALKWNAHLKQEIQAALQEQ 28

RESULT 5
AAB74356
ID AAB74356 standard; peptide; 28 AA.
XX AC
XX AAB74356;
XX 02-JUL-2001 (first entry)
XX Peptide used to form blunt-ended heterodimers.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-GB003576.
XX 17-SEP-1999; 99GB-00022013.
XX (UYSU-) UNIV SUSSEX.
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX Claim 16; Page 26; 45pp; English.
XX The present invention relates to a protein structure with several first
XX peptide monomer units arranged in a first strand and several second
XX peptide monomer units arranged in a second strand. The structure is
XX useful in Atomic Force Microscopy and a number of other applications. The
XX present sequence is the peptide monomer unit SAF-p2
XX Sequence 28 AA;

Query Match      89.8%; Score 123; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.7e-09;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIQAALQEQ 28
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 KIRALKWNAHLKQEIQAALQEQ 28

RESULT 7
AAB74345
ID AAB74345 standard; peptide; 28 AA.
XX AC
XX AAB74345;
XX 02-JUL-2001 (first entry)
XX Peptide SAF-p2A.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-GB003576.
XX 17-SEP-1999; 99GB-00022013.
XX (UYSU-) UNIV SUSSEX.
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX Disclosure; Page 9; 45pp; English.

SQ Sequence 28 AA;

Query Match      89.8%; Score 123; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 2.7e-09;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIQAALQEQ 28
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 KIRALKWNAHLKQEIQAALQEQ 28

RESULT 6
AAB74352
ID AAB74352 standard; peptide; 28 AA.
XX AC
XX AAB74352;
XX 02-JUL-2001 (first entry)
XX Peptide SAF-p2.
XX Atomic Force Microscopy; AFM.
```

XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p2A
XX
SQ Sequence 28 AA;

Query Match 89.1%; Score 122; DB 4; Length 28;
Best Local Similarity 92.9%; Pred. No. 3.7e-09;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLKQEIATALEQIEIAALEQ 28
DB 1 KIRALKWKNHLKQEIATALEQIEIAALEQ 28

RESULT 8
ADM41438
ID ADM41438 standard; peptide; 28 AA.
XX
AC ADM41438;
XX
DT 03-JUN-2004 (first entry)
XX
DE Self-assembling peptide fibre SAF-p2a.
XX
KW Fibre-shaping peptide; self-assembling peptide.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal NH3 moiety"
FT
XX
PN WO2004022584-A1.
XX
PD 18-MAR-2004.

XX
XX 08-SEP-2003; 2003WO-GB003900.
XX
XX 06-SEP-2002; 2002GB-00020805.
XX
XX (UYSU-) UNIV SUSSEX.
XX
XX Woolfson D, Ryadnov MG;
XX
XX WPI; 2004-248444/23.

XX Novel fiber-shaping peptide comprising hub and several peptide monomer
PT units, useful for producing protein structure useful in purification of
PT biological fluids and in surface engineering procedures.
XX
PS Example 36; Page 22; 37pp; English.

XX The present sequence is that of self-assembling peptide fibre (SAF) SAF-
CC p2a. The invention relates to fibre-shaping (Fish) peptides ADM41434-
CC ADM41435 that are capable of interacting with SAFs to form protein
CC structures. The Fish peptides allow morphological changes (branches,
CC splits, kinks and bends) to be made to protein fibres comprising SAFs. By
CC incorporating such morphological changes in the protein fibres, it is
CC possible to generate a variety of (nanoscale) protein structures, such as
CC assemblies in general, including matrix, filter, network, grid and
CC scaffold structures. Use of the protein structures in the purification of
CC biological fluids, for assembling cells for cell and tissue engineering,
CC and in surface engineering procedures is claimed.

XX Sequence 28 AA;

Query Match 76.6%; Score 105; DB 8; Length 28;
Best Local Similarity 85.7%; Pred. No. 6.8e-07;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLKQEIATALEQIEIAALEQ 28
DB 1 KIRALKWKNHLKQEIATALEQIEIAALEQ 28
RESULT 9
ABR84737
ID ABR84737 standard; peptide; 28 AA.
XX
AC ABR84737;
XX
DT 18-DEC-2003 (first entry)
XX
DE DE novo designed AHEC peptide #5.
XX
KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KW AHEC; antiparallel; drug targeting.
XX
OS Synthetic.
XX
PN WO2003066660-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001217.
XX
PR 05-FEB-2002; 2002US-0354376P.
XX
PA (IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX
PI Caterer NR, Uttental LO, Neilson RW;
XX
DR WPI; 2003-679535/64.
XX
PT Composition useful for forming therapeutic antibodies and antibody
PT fragments comprises pair of antibody Fv fragments linked and stabilized
PT by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX
PS Disclosure; Page 14; 35pp; English.

XX The present invention relates to a composition which comprises a pair of
CC antibody Fv fragments linked and stabilised by antiparallel heterogeneous
CC alpha-helical coiled-coil (AHEC) peptides. The composition is used to
CC form multimeric complexes and therapeutic antibodies and antibody
CC fragments useful for e.g. inhibition of receptor binding and the
CC targeting of drugs, toxins and labels in research, industry and
CC healthcare. The present sequence is an AHEC peptide used in the
CC exemplification of the invention
XX
SQ Sequence 28 AA;

Query Match 59.1%; Score 81; DB 7; Length 28;
Best Local Similarity 64.0%; Pred. No. 0.0011;
Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 ALKWKNNHLKQEIATALEQIEIAALEQ 28
DB 1 AIKYQQAIAIKNEIAATKQEIATALEQ 25

RESULT 10
AAB74343
ID AAB74343 standard; peptide; 28 AA.
XX
AC AAB74343;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p1C.
XX
KW Atomic Force Microscopy; AFM.
XX

OS Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX PD
 XX PF 18-SEP-2000; 2000WO-GB003576.
 XX PR 17-SEP-1999; 99GB-00022013.
 XX PA (UYSU-) UNIV SUSSEX.
 XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX DR
 XX PT New protein structures with peptide monomer units, useful in Atomic Force
 XX PT Microscopy, purifying biological fluids, promoting tissue repair and
 XX PT tissue engineering, or constructing nanoscale molecular sieves.
 XX PS Claim 16; Page 26; 45pp; English.
 XX CC The present invention relates to a protein structure with several first
 XX CC peptide monomer units arranged in a first strand and several second
 XX CC peptide monomer units arranged in a second strand. The structure is
 XX CC useful in Atomic Force Microscopy and a number of other applications. The
 XX CC present sequence is the peptide monomer unit SAF-plc
 XX SQ Sequence 28 AA;
 Query Match 54.7%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0069;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 XX
 OY 1 KIRALKWNAHLKQEIATALEQ 28
 |||||
 DB 1 KIRALKQKIASLKQEIATALEQ 28
 |||||
 RESULT 11
 AAB74351
 ID AAB74351 standard; peptide; 28 AA.
 XX AC AAB74351;
 XX DT 02-JUL-2001 (first entry)
 XX DE Peptide SAF-pl.
 XX KW Atomic Force Microscopy; AFM.
 XX OS Unidentified.
 XX PN WO200121646-A1.
 XX PD 29-MAR-2001.
 XX PF 18-SEP-2000; 2000WO-GB003576.
 XX PR 17-SEP-1999; 99GB-00022013.
 XX PA (UYSU-) UNIV SUSSEX.
 XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX DR
 XX PT New protein structures with peptide monomer units, useful in Atomic Force
 XX PT Microscopy, purifying biological fluids, promoting tissue repair and
 XX PT tissue engineering, or constructing nanoscale molecular sieves.
 XX PS Claim 16; Page 26; 45pp; English.
 XX

CC The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-pl
 XX SQ Sequence 28 AA;
 Query Match 54.7%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0069;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 XX
 OY 1 KIRALKWNAHLKQEIATALEQ 28
 |||||
 DB 1 KIRALKQKIASLKQEIATALEQ 28
 |||||
 RESULT 12
 ADM41436
 ID ADM41436 standard; peptide; 28 AA.
 XX AC ADM41436;
 XX DT 03-JUN-2004 (first entry)
 XX DE Self-assembling peptide fibre SAF-pl.
 XX KW Fibre-shaping peptide; self-assembling peptide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1 /note= "N-terminal NH3 moiety"
 XX PN WO2004022584-A1.
 XX PD 18-MAR-2004.
 XX PF 08-SEP-2003; 2003WO-GB003900.
 XX PR 06-SEP-2002; 2002GB-00020805.
 XX PA (UYSU-) UNIV SUSSEX.
 XX PI Woolfson D, Ryadnov MG;
 XX WPI; 2004-248444/23.
 XX DR
 XX PT Novel fiber-shaping peptide comprising hub and several peptide monomer
 XX PT units, useful for producing protein structure useful in purification of
 XX PT biological fluids and in surface engineering procedures.
 XX PS Example 30; Page 22; 37pp; English.
 XX CC The present sequence is that of self-assembling peptide fibre (SAF) SAF-
 XX CC pl. The invention relates to fibre-shaping (Fish) peptides ADM41434-
 XX CC ADM41435 that are capable of interacting with SAFs to form protein
 XX CC structures. The Fish peptides allow morphological changes (branches,
 XX CC splits, kinks and bends) to be made to protein fibres comprising SAFs. By
 XX CC incorporating such morphological changes in the protein fibres, it is
 XX CC possible to generate a variety of (nanoscale) protein structures, such as
 XX CC assemblies in general, including matrix, filter, network, grid and
 XX CC scaffold structures. Use of the protein structures in the purification of
 XX CC biological fluids, for assembling cells for cell and tissue engineering,
 XX CC and in surface engineering procedures is claimed.
 XX SQ Sequence 28 AA;
 Query Match 54.7%; Score 75; DB 8; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0069;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 XX

```

QY 1 KIPALKKWAHLKQETAALEQ 28
Db 1 KIAALKQKIAALKQETAALEQ 28

RESULT 13
AAB74341
ID AAB74341 standard; peptide; 28 AA.
XX AC AAB74341;
XX 02-JUL-2001 (first entry)
XX Peptide SAF-plA.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-GB003576.
XX 17-SEP-1999; 99GB-00022013.
XX (UYSU-) UNIV SUSSEX.
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX Disclosure; Page 9; 45pp; English.
XX The present invention relates to a protein structure with several first
XX peptide monomer units arranged in a first strand and several second
XX peptide monomer units arranged in a second strand. The structure is
XX useful in Atomic Force Microscopy and a number of other applications. The
XX present sequence is the peptide monomer unit SAF-plA
XX Sequence 28 AA;

Query Match 54.0%; Score 74; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0094;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIPALKKWAHLKQETAALEQ 28
Db 1 KIAALKQKIAALKQETAALEQ 28

RESULT 15
AAB74355
ID AAB74355 standard; peptide; 28 AA.
XX AC AAB74355;
XX 02-JUL-2001 (first entry)
XX Peptide used to form blunt-ended heterodimers.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-GB003576.
XX 17-SEP-1999; 99GB-00022013.
XX (UYSU-) UNIV SUSSEX.
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX Disclosure; Fig 8; 45pp; English.
XX The present invention relates to a protein structure with several first
XX peptide monomer units arranged in a first strand and several second
XX peptide monomer units arranged in a second strand. The structure is
XX useful in Atomic Force Microscopy and a number of other applications. The
XX present sequence is a peptide used to form blunt-ended heterodimers.
XX Sequence 28 AA;

Query Match 54.0%; Score 74; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0094;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIPALKKWAHLKQETAALEQ 28
Db 1 KIAALKQKIAALKQETAALEQ 28

RESULT 14
AAB74342
ID AAB74342 standard; peptide; 28 AA.
XX AC AAB74342;
XX 02-JUL-2001 (first entry)
XX Peptide SAF-plB.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.

```

KW	Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KX	AHEC; antiparallel; drug targeting.
XW	Synthetic.
XX	WO2003066660-A2.
XX	14-AUG-2003.
XX	05-FEB-2003; 2003WO-EP001217.
XX	05-FEB-2002; 2002US-0354376P.
PR	(IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX	Caterer NR, Uttental LO, Neilson RW;
PA	WIPI; 2003-679535/64.
XX	Composition useful for forming therapeutic antibodies and antibody fragments comprises pair of antibody Fv fragments linked and stabilized by antiparallel heterogeneous alpha-helical coiled-coil peptides.
PT	Disclosure; Page 14; 35pp; English.
XX	The present invention relates to a composition which comprises a pair of antibody Fv fragments linked and stabilised by antiparallel heterogeneous alpha-helical coiled-coil (AHEC) peptides. The composition is used to form multimeric complexes and therapeutic antibodies and antibody fragments useful for e.g. inhibition of receptor binding and the targeting of drugs, toxins and labels in research, industry and healthcare. The present sequence is an AHEC peptide used in the exemplification of the invention
CC	Sequence 28 AA;
XX	
SQ	
Query Match	43.1%; Score 59; DB 7; Length 28;
Best Local Similarity	40.0%; Pred.No. 0.94;
Matches	10; Conservative 12; Mismatches 3; Indels 0; Gaps 0
Oy	4 ALKWNHLKQETAAALEQTAALEQ 28 ::: : ::: :::
Dd	1 AIEYEQAIKEETAARKIAIKE 25 ::: : ::: :::
RESULT 18	
ABR84736	
ID	ABR84736 standard; peptide; 28 AA.
XX	
AC	ABR84736;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	De novo designed AHEC peptide #4.
XX	
KW	Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KX	AHEC; antiparallel; drug targeting.
XX	Synthetic.
OS	
XX	WO2003066660-A2.
PN	
PD	14-AUG-2003.
XX	
PF	05-FEB-2003; 2003WO-EP001217.
XX	
XX	05-FEB-2002; 2002US-0354376P.
' , XX	
PA	(IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX	Caterer NR, Uttental LO, Neilson RW;
FI	
DR	WIPI; 2003-679535/64

XX Composition useful for forming therapeutic antibodies and antibody
PT fragments comprises pair of antibody Fv fragments linked and stabilized
PT by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX
PS Disclosure; Page 14; 35pp; English.
XX
CC The present invention relates to a composition which comprises a pair of
CC antibody Fv fragments linked and stabilised by antiparallel heterogeneous
CC alpha-helical coiled-coil (AHEC) peptides. The composition is used to
CC form multimeric complexes and therapeutic antibodies and antibody
CC fragments useful for e.g. inhibition of receptor binding and the
CC targeting of drugs, toxins and labels in research, industry and
CC healthcare. The present sequence is an AHEC peptide used in the
CC exemplification of the invention
XX
SQ Sequence 28 AA;

Query Match 39.4%; Score 54; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.4;
Matches 12; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQETIALEQETA 24
Db 5 KIAAIEKIAQIEETIAAQEKIA 28

RESULT 19
AAU14021
ID AAU14021 standard; peptide; 28 AA.
XX
AC AAU14021;
XX
DT 21-NOV-2001 (first entry)
XX
DE Peptide sequence from yeast GCN4.
XX
KW Anti-retroviral; DP178-like; DP107-like; antifusogenic; antiviral;
KW HIV transmission; GCN4; Yeast.
XX
OS Saccharomyces sp.
XX
XX WO200151673-A2.
PN
XX 19-JUL-2001.
PD
XX
XX 05-JUL-2000; 2000WO-US035727.
PF
XX
XX 09-JUL-1999; 99US-00350841.
PR
XX (TRIM-) TRIMERIS INC.
PA
XX
PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX
XX WPI; 2001-442157/47.
DR
XX
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX
XX Disclosure; Fig 12; 259pp; English.
PS
XX
XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and

CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from yeast GCN4
XX
SQ Sequence 28 AA;

Query Match 32.8%; Score 45; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 70;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQETIALEQ 21
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 20
ABO10240
ID ABO10240 standard; peptide; 28 AA.
XX
AC ABO10240;
XX
DT 19-AUG-2003 (first entry)
XX
DE Heptad repeat containing region of yeast GCN4.
XX
KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX
OS Saccharomyces cerevisiae.
XX
XX US6518013-B1.
PN
XX 11-FEB-2003.
PD
XX
XX 07-JUN-1995; 95US-00495546.
PF
XX 07-JUN-1993; 93US-00073028.
PR
XX 07-JUN-1994; 94US-00255208.
PR
XX 20-DEC-1994; 94US-00360107.
XX
XX (TRIM-) TRIMERIS INC.
PA
XX
XX Barney SO, Lambert DM, Petteway SR;
PI
XX WPI; 2003-465599/44.
DR
XX
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX
XX Example; Fig 12; 716pp; English.
PS
XX
XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of ALLMOT15,
CC 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amido group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a heptad

AC ADY52132;
XX 19-MAY-2005 (first entry)
XX Heparin binding protein associated amino acid sequence, SEQ ID NO:65.
XX heparin binding protein; assay; heparin; anticoagulant; blood-clotting.
XX heparin binding protein; assay; heparin; anticoagulant; blood-clotting.
XX Unidentified.
XX WO2005018552-A2.
XX 03-MAR-2005.
XX 12-AUG-2004; 2004WO-US026066.
XX 12-AUG-2003; 2003US-0494495P.
XX (UTAH) UNIV UTAH RES FOUND.
XX Prestwich GD, Shenshen C, Beattie J, Mostert MJ;
XX WPI; 2005-214150/22.
XX New composition comprising a heparin binding molecule (HBM) having a
XX heparin binding unit (HBU), useful in neutralizing heparin in a subject.
XX Disclosure; SEQ ID NO 65; 152pp; English.
XX The invention relates to a new composition comprising a heparin binding
XX molecule (HBM) having a heparin binding unit (HBU). Also described are
XX (i) a nucleic acid comprising a sequence encoding a heparin-binding
XX molecule (HBM) nucleic acid, (ii) an assay for detecting heparin, (iii) a
XX method for determining the amount of heparin in a sample, (iv) a method
XX of detecting heparin, (v) a method of removing heparin from a sample,
XX (vi) a method for detecting heparin on coated surfaces, (vii) a kit
XX comprising a HBM, color developing reagent, control standards, wash
XX buffer and instructions, (viii) an apparatus comprising a medical device
XX coated with HBM, (ix) a method of manufacturing a medical device, and (x)
XX a method of neutralizing heparin in a subject. The composition further
XX comprises a linker and a second HBU and a second linker and a third HBU.
XX The heparin-binding unit comprises a peptide having at least 80% identity
XX to a fully defined sequence 62-amino acid sequence (SEQ ID NO: 6). The
XX first, second and third HBU comprise a fully defined 9-amino acid
XX sequence (SEQ ID NO: 1). The HBM is fused to a bacterial glutathione-S-
XX transferase (GST). The GST-HBM is also fused to a bacterial alkaline
XX phosphatase (BAP). The GST-HBM is also fused to an enhanced green
XX fluorescent protein (EGFP). The composition is useful in neutralizing
XX heparin in a subject. This sequence represents an amino acid sequence
XX relating to the present invention.
XX Sequence 28 AA;
Query Match 29.9%; Score 41; DB 9; Length 28;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 5 LKWNNAHLKOEIAALEQIEIAALEQ 28
DB 3 LXDENSLKSEVSKLSQLVKKQ 26
RESULT 26
AAB50879
ID AAB50879 standard; peptide; 28 AA.
XX AC AAB50879;
XX DT 19-MAR-2001 (first entry)
XX DE Integrin cytoplasmic domain heptad-repeat.
XX DT Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin;
XX KW Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin;
KW immunosuppressive; inflammatory bowel disease; arthritis;
KW multiple sclerosis; asthma; atherosclerosis; wound healing;
XX cytoplasmic domain; heptad-repeat.
OS Homo sapiens.
XX WO200073342-A1.
PN 07-DEC-2000.
PD 01-JUN-2000; 2000WO-US015153.
PF 01-JUN-1999; 99US-00323447.
PR (SCRI) SCRIPPS RES INST.
XX Ginsberg MH, Pfaff M, Liu S;
XX WPI; 2001-070959/08.
XX Polypeptides useful in construction of structural models for identifying
XX therapeutic compounds, comprises series of heptad repeats that mimic a
XX transmembrane domain and cytoplasmic domain attached to heptad repeats.
XX Example 2; Fig 1A; 37pp; English.
XX The present sequence is given in a specification relating to a
XX polypeptide comprising a series of heptad-repeats that mimic a
XX transmembrane domain, and a selected cytoplasmic domain attached to the
XX heptad repeats. At least a portion of the polypeptide is prepared
XX recombinantly or at least 1 heptad repeat in the series has a different
XX amino acid sequence to other heptad repeats in the series. The
XX polypeptide is useful in the construction of structural models which are
XX useful for evaluating structure and activity of a selected cytoplasmic domain
XX clustered transmembrane protein having the selected cytoplasmic domain
XX and for identifying therapeutic compounds. It is also useful for
XX identifying agents as inhibitors of alpha4 integrin biological responses
XX by contacting the structural model with paxillin or a paxillin related
XX molecule in the presence and absence of a test agent and determining
XX binding of paxillin or paxillin related molecule to the structural model.
XX A decrease in binding in the presence of the test agent indicates that
XX the test agent is an inhibitor of alpha4 integrin biological response.
XX Inhibitors of the binding of paxillin to alpha4 are useful in blocking
XX immune responses in conditions such as inflammatory bowel disease,
XX arthritis, multiple sclerosis and asthma and in inhibiting
XX atherosclerosis and scarring during wound healing
XX Sequence 28 AA;
Query Match 28.5%; Score 39; DB 4; Length 28;
Best Local Similarity 37.0%; Pred. No. 4.4e+02;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY 1 KIRALKWNAHLKOEIAALEQIEIAALE 27
DB 1 KLEALEGRLEDALEKLEALEKLEDALE 27
RESULT 27
AAB59138
ID AAB59138 standard; peptide; 28 AA.
XX AC AAB59138;
XX DT 21-MAR-2001 (first entry)
XX DE Alpha-helical heptad repeat.
XX DT Heptad repeat; transmembrane domain; cytoplasmic; integrin; inflammation;
XX KW thrombosis; malignancy.
XX OS Synthetic.
XX


```
Query Match      27.7%; Score 38; DB 6; Length 28;
Best Local Similarity 24.0%; Pred. No. 6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKOEIAALEOEIAA 25
Db 4 KUKAMEEKLKAMEEKLKAMEEKLKA 28

RESULT 32
ABO44343
ID ABO44343 standard; peptide; 28 AA.
XX
AC ABO44343;
XX
DT 25-SEP-2003 (first entry)
XX
DE Ear 1-based lysine-rich heptad repeat SSP(7)4.
XX
KW Aspartokinase; AKIII; dihydrodipicolinic acid synthase; DHDPS;
KW seed lysine content; seed threonine content; seed storage protein; SSP;
KW chloroplast transit sequence; lysine-rich protein;
KW lysine ketoglutarate reductase; LKR; transgenic.
XX
OS Synthetic.
XX
PN US2003056242-A1.
XX
PD 20-MAR-2003.
XX
PF 17-DEC-2001; 2001US-00023066.
XX
PR 19-MAR-1992; 92US-00855414.
PR 18-MAR-1993; 93WO-US002480.
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 24-MAR-1997; 97US-00823771.
XX
PA (FALC/) FALCO S C.
XX
PI Falco SC;
XX
DR WPI; 2003-521869/49.
DR N-PSDB; ACH03709.
XX
PT New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic
PT acid synthase, useful for increasing threonine or lysine content of seeds
PT of plant.
XX
PS Example 21; Page 44; 116pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment comprising a
CC first nucleic acid subfragment encoding aspartokinase (AK) that is
CC substantially insensitive to inhibition by lysine, and a second nucleic
CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDPS) that
CC is substantially insensitive to inhibition by lysine. Also included are
CC an isolated nucleic acid fragment comprising a nucleic acid subfragment
CC encoding lysine ketoglutarate reductase (LKR), a chimaeric gene (where
CC the nucleic acid fragment is operably linked to a plant chloroplast
CC transit sequence and to a seed-specific regulatory sequence, a plant
CC comprising the nucleic acid/chimaeric gene in its genome, a seed obtained
CC from the plant, increasing threonine or lysine content of the seeds of
CC plant, a plant capable of transmitting the chimaeric gene to a progeny of
CC plant having the ability to produce levels of free threonine or lysine at
CC least two times greater than the free threonine levels of untransformed
CC plants, a transformed (soybean) plant comprising seeds that accumulate
CC lysine at a level at least ten percent to four-fold higher than the seeds
CC of an untransformed plant, a transformed rapeseed comprising seeds that
CC accumulate lysine to a level between ten percent and one hundred percent
CC higher than that of the seeds of an untransformed plant, a monocot plant
CC comprising in its genome the nucleic acid fragment having the monocot-
CC embryo specific promoter and a transformed corn plant comprising seeds
CC that accumulate lysine to a level between ten percent and one hundred
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CC thirty percent higher than the seeds of the untransformed plant. Also
CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up
CC from monomer lysine-rich heptad repeats (encoded by Ear1 restriction
CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed
CC plant. The nucleic acid fragments, genes and methods are useful for
CC increasing threonine or lysine content of the seeds of the plant. Seeds
CC containing increased threonine or lysine content eliminate the need to
CC supplement mixed grain feeds with lysine or threonine produced via
CC microbial fermentation. The present sequence is a lysine-rich heptad
CC repeat for use as a monomer unit in a synthetic seed storage protein
XX
SQ Sequence 28 AA;

Query Match      27.7%; Score 38; DB 6; Length 28;
Best Local Similarity 24.0%; Pred. No. 6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKOEIAALEOEIAA 25
Db 4 KUKAMEEKLKAMEEKLKAMEEKLKA 28

RESULT 33
ADW71693
ID ADW71693 standard; peptide; 28 AA.
XX
AC ADW71693;
XX
DT 24-MAR-2005 (first entry)
XX
DE Peptide SSP(7)4 SEQ ID NO:70.
XX
KW transgenic plant; amino acid production; seed; enzyme engineering.
XX
OS Synthetic.
XX
PN US2005005330-A1.
XX
PD 06-JAN-2005.
XX
PF 19-MAR-2004; 2004US-00804678.
XX
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 27-MAR-1997; 97US-00824627.
PR 27-MAR-1998; 98US-00049304.
XX
PA (FALC/) FALCO S C.
PA (MCDE/) MCDEVITT R E.
PA (EPEL/) EPELBAUM S U.
XX
PI Falco SC, Mcdevitt RE, Epelbaum SU;
XX
DR WPI; 2005-065280/07.
DR N-PSDB; ADW71691.
XX
PT New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase
PT nucleic acid fragment, useful for increasing levels of lysine in the
PT seeds of transformed plants.
XX
PS Example 21; SEQ ID NO 70; 142pp; English.
XX
CC The invention relates to a novel isolated nucleic acid sequence which is
CC useful in antisense inhibition or sense suppression of endogenous lysine
CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn
CC plant or corn plant cell, where the isolated nucleic acid fragment
CC comprises all or a part of a nucleic acid sequence (ADW71743). The
CC isolated nucleic acid fragment is useful for increasing levels of lysine
CC in the seeds of transformed plants. The present sequence represents a
CC peptide encoded by an oligonucleotide used to create chimeric genes of
CC the invention.
XX
SQ Sequence 28 AA;
```

```

Query Match      27.7%; Score 38; DB 9; Length 28;
Best Local Similarity 24.0%; Pred. No. 6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIRALKWNHKLKQEIALLQEIATA 25
Db 4 KIKAMEEKLKAMEEKLKAMEEKLKA 28

RESULT 34
AAR34576
ID AAR34576 standard; protein; 28 AA.
XX
AC AAR34576;
XX
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-JUN-1993 (first entry)
XX
XX Domain 1 from integrase like protein Rci.
DE cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG;
XX Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV; pertussis;
KW malaria; influenza virus; CTL; herpes virus.
XX Borrelia burgdorferi.
XX
XX W09307897-A1.
XX
XX 29-APR-1993.
XX
XX 21-OCT-1992; 92WO-US009075.
XX
XX 21-OCT-1991; 91US-00780261.
XX
XX (MEDI-) MEDIMUNE INC.
XX
XX Stover CK;
XX
XX WPI; 1993-152187/18.
XX
XX Expression vector for expressing protein or polypeptide in mycobacterium
PT - contg DNA sequences encoding lipoprotein secretion signal and peptide
PT heterologous to bacteria expressing fusion protein of lipoprotein
PT heterologous to bacteria.
XX
XX Disclosure; Fig 29; 86pp; English.
XX
XX This sequence is domain 1 from the integrase like protein Rci. The whole
CC coding sequence of the enzyme could be included in an expression vector
CC in order to aid its integration into its host. The expression vector also
CC includes at least the secretion signal of a lipoprotein and a second
CC sequence encoding a heterologous protein and a mycobacterial promoter to
CC control expression of the heterologous protein. (Updated on 09-JAN-2003
CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 28 AA;

Query Match      27.0%; Score 37; DB 2; Length 28;
Best Local Similarity 56.2%; Pred. No. 8.1e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 11 HLKQEIALLQEIATA 26
Db 5 HLALETAMRQEIALL 20

RESULT 35
AAR32693
ID AAR32693 standard; protein; 28 AA.
XX
AC AAR32693;

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```

XX
DT 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
XX
XX SSP polypeptide produced from clone 84-H3.
DE Heptad; plants; custom tailored storage proteins; in vivo; expression.
XX
XX Synthetic.
OS
XX W09303160-A1.
XX
XX 18-FEB-1993.
XX
XX 07-AUG-1992; 92WO-US006412.
XX
XX 09-AUG-1991; 91US-00743006.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, Keeler SJ, Rice JA;
XX
XX WPI; 1993-076517/09.
DR N-PSDB; AAQ37274.
XX
XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.
XX
XX Disclosure; Page 124; 176pp; English.
XX
XX The sequence represents a synthetic heptad polypeptide which can be
CC expressed in vivo in plants to serve as a synthetic seed storage protein
CC which can be custom-tailored for specific end-user requirements. The DNA
CC encoding the heptad may be used to transform plants to increase the
CC content of partic. amino acids such as lysine or methionine in seeds or
CC leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 28 AA;

Query Match      26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIRALKWNHKLKQEIALLQEIATA 25
Db 4 KIKAMEEKLKAMEEKLKAMEEKLKA 28

RESULT 36
AAR32689
ID AAR32689 standard; peptide; 28 AA.
XX
XX AAR32689;
AC
XX
XX 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
XX
XX SSP polypeptide produced from clone D16.
DE Heptad; plants; custom tailored storage proteins; in vivo; expression.
XX
XX Synthetic.
OS
XX W09303160-A1.
XX
XX 18-FEB-1993.
XX
XX 07-AUG-1992; 92WO-US006412.
XX
XX 09-AUG-1991; 91US-00743006.
XX
XX

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PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1993-076517/09.
DR N-PSDB; AAQ37270.
XX
PT Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.
XX
PS Disclosure; Page 120; 176pp; English.
XX
CC The sequence represents a synthetic heptad polypeptide which can be
CC expressed in vivo in plants to serve as a synthetic seed storage protein
CC which can be custom-tailored for specific end-user requirements. The DNA
CC encoding the heptad may be used to transform plants to increase the
CC content of partic amino acids such as lysine or methionine in seeds or
CC leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 1 KIRALKWNAHLKQETAALEQETAA 25
|::|::| ::::|:|::|
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28
|::|::| ::::|:|::|

RESULT 37
AAR31980
ID AAR31980 standard; peptide; 28 AA.
XX
AC AAR31980;
XX
DT 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
XX
DE SSP5 polypeptide, suitable for in vivo expression.
XX
KW Heptad; plants; custom tailored storage proteins.
XX
OS Synthetic.
XX
PN WO9303160-A1.
XX
PD 18-FEB-1993.
XX
PF 07-AUG-1992; 92WO-US006412.
XX
PR 09-AUG-1991; 91US-00743006.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1993-076517/09.
XX
CC Synthetic polypeptide(s) contg. specified heptad units - expressed in
CC vivo in plants to serve as custom-tailored storage proteins with
CC specified aminoacid content.
XX
PS Claim 7; Page 102; 176pp; English.
XX
CC The sequence represents a synthetic polypeptide comprising heptad units
CC of the peptide. The synthetic polypeptide can be expressed in vivo in
CC plants to serve as a synthetic seed storage protein which can be custom-
CC tailored for specific end-user requirements. The DNA encoding the heptad
CC may be used to transform plants to increase the content of partic. amino
CC acids such as lysine or methionine in seeds or leaves. See also AAR31979-
CC
```

```
CC 86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 1 KIRALKWNAHLKQETAALEQETAA 25
|::|::| ::::|:|::|
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28
|::|::| ::::|:|::|

RESULT 38
AAR78255
ID AAR78255 standard; peptide; 28 AA.
XX
AC AAR78255;
XX
DT 15-JUL-1996 (first entry)
XX
DE SSP(5) 4 heptad.
XX
KW Lysine; synthetic storage protein; SSP; Vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
KW Glycine max; transgenic plant; essential amino acid.
XX
OS Synthetic.
XX
PN WO9515392-A1.
XX
PD 08-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US013190.
XX
PR 30-NOV-1993; 93US-00160117.
PR 17-JUN-1994; 94US-00261661.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1995-215272/28.
DR N-PSDB; AAQ94998.
XX
PT New chimeric gene providing increased lysine content in plant seeds -
PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of
PT improved nutritional value.
XX
PS Example 8; Page 81; 180pp; English.
XX
CC Oligonucleotide SM96 (AAQ94998) and complementary sequence SM97
CC (AAQ94999) code for 4 repeats (AAR78255) of heptad peptide SSP5 (see also
CC AAR78238). Clone 3-5 (AAQ95006) was obt'd. by insertion of the first 22
CC bases of the SM96-SM97 set into the EarI site of clone 82-4 (see
CC AAQ94992) and transformation of Escherichia coli DHS alpha. Synthetic
CC storage protein SSP3-5 (AAR78260) encoded by the construct was used to
CC raise the lysine content in seeds of transformed tobacco, soybean and
CC corn
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 1 KIRALKWNAHLKQETAALEQETAA 25
|::|::| ::::|:|::|
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28
|::|::| ::::|:|::|

RESULT 39
```

```

AAR78250
ID AAR78250 standard; protein; 28 AA.
XX
XX AC AAR78250;
XX
XX DT 15-JUL-1996 (first entry)
XX
XX DE SSP 5.5.5.5.
XX
XX Lysine; synthetic storage protein; SSP; vector; pSK6;
XX dihydrodipicolinic acid synthase; corn; maize; soybean;
XX Glycine max; transgenic plant; essential amino acid.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FH Peptide 1..7
XX FT /label= SSP5
XX FT Peptide 8..14
XX FT /label= SSP5
XX FT Peptide 15..21
XX FT /label= SSP5
XX FT Peptide 22..28
XX FT /label= SSP5
XX
XX FN W09515392-A1.
XX
XX PD 08-JUN-1995.
XX
XX PF 21-NOV-1994; 94WO-US013190.
XX
XX PR 30-NOV-1993; 93US-00160117.
XX PR 17-JUN-1994; 94US-00261661.
XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX PI Falco SC, Keeler SJ, Rice JA;
XX
XX DR WPI; 1995-215272/28.
XX
XX N-PSDB; AAQ94993.
XX
XX New chimeric gene providing increased lysine content in plant seeds -
XX contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX transport sequence and seed specific promoter, also new plants of
XX improved nutritional value.
XX
XX Example 8; Page 136; 180pp; English.
XX
XX Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78250) comprises 2
XX heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
XX derived from vector pSK6. It was obtd. by insertion of HPLC-purified SSP5
XX -encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the
XX resulting vector to transform Escherichia coli JM103, yielding clone 84-
XX H3 (AAQ94993). The SSP forms a coiled-coil structure. It can be expressed
XX in the seeds of transformed plants, e.g. soybean and corn, to increase
XX lysine content
XX
XX Sequence 28 AA;
XX
XX Query Match 26.3%; Score 36; DB 2; Length 28;
XX Best Local Similarity 24.0%; Pred. No. 1.1e+03;
XX Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 KIRALKWKNKHLKQETIAAEQETIAA 25
XX |:::| |:::| |:::| |:::|
XX 4 KMKAMEEKWKAMEEKWKAMEEKWKMA 28
XX
XX RESULT 40
XX AAR78244
XX ID AAR78244 standard; protein; 28 AA.
XX
XX AC AAR78244;

```

```

XX
XX DT 15-JUL-1996 (first entry)
XX
XX DE SSP 5.5.5.5.
XX
XX Lysine; synthetic storage protein; SSP; vector; pSK6;
XX dihydrodipicolinic acid synthase; corn; maize; soybean;
XX Glycine max; transgenic plant; essential amino acid.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FH Peptide 1..7
XX FT /label= SSP5
XX FT Peptide 8..14
XX FT /label= SSP5
XX FT Peptide 15..21
XX FT /label= SSP5
XX FT Peptide 22..28
XX FT /label= SSP5
XX
XX FN W09515392-A1.
XX
XX PD 08-JUN-1995.
XX
XX PF 21-NOV-1994; 94WO-US013190.
XX
XX PR 30-NOV-1993; 93US-00160117.
XX PR 17-JUN-1994; 94US-00261661.
XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX PI Falco SC, Keeler SJ, Rice JA;
XX
XX DR WPI; 1995-215272/28.
XX
XX N-PSDB; AAQ94983.
XX
XX New chimeric gene providing increased lysine content in plant seeds -
XX contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX transport sequence and seed specific promoter, also new plants of
XX improved nutritional value.
XX
XX Example 8; Page 129; 180pp; English.
XX
XX Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78244) comprises 2
XX heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
XX derived from vector pSK6. It was obtd. by insertion of SSP5-encoding
XX oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector
XX to transform Escherichia coli JM103, yielding clone D33 (AAQ94983). The
XX SSP forms a coiled-coil structure. It can be expressed in the seeds of
XX transformed plants, e.g. soybean and corn, to increase lysine content
XX
XX Sequence 28 AA;
XX
XX Query Match 26.3%; Score 36; DB 2; Length 28;
XX Best Local Similarity 24.0%; Pred. No. 1.1e+03;
XX Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 KIRALKWKNKHLKQETIAAEQETIAA 25
XX |:::| |:::| |:::| |:::|
XX 4 KMKAMEEKWKAMEEKWKAMEEKWKMA 28
XX
XX Db
XX
XX RESULT 41
XX AAR78242
XX ID AAR78242 standard; protein; 28 AA.
XX
XX AC AAR78242;
XX
XX DT 15-JUL-1996 (first entry)
XX
XX DE SSP 5.5.5.5.
XX
XX

```

KW Lysine; synthetic storage protein; SSP; vector; PSK6;
 KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
 KW Glycine max; transgenic plant; essential amino acid.

XX Synthetic.

XX Key Location/Qualifiers
 FH Peptide 1..7 /label= SSP5
 FT Peptide 8..14 /label= SSP5
 FT Peptide 15..21 /label= SSP5
 FT Peptide 22..28 /label= SSP5

FT WO9515392-A1.

XX 08-JUN-1995.

XX 21-NOV-1994; 94WO-US013190.

XX 10-NOV-1993; 93US-00160117.

PR 17-JUN-1994; 94US-00261661.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Keeler SJ, Rice JA;

XX WPI; 1995-215272/28.

DR N-PSDB; AAQ94981.

XX New chimeric gene providing increased lysine content in plant seeds -
 PT contains dihydrodipicolinic acid synthase gene coupled to chloroplast
 PT transposon sequence and seed specific promoter, also new plants of
 PT improved nutritional value.

XX Example 8; Page 127; 180pp; English.

XX Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78242) comprises 2
 CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
 CC derived from vector PSK6. It was obtd. by insertion of SSP5-encoding
 CC oligonucleotides (AAQ94974-75) into PSK6 and use of the resulting vector
 CC to transform Escherichia coli JM103, yielding clone D16 (AAQ94981). The
 CC SSP forms a coiled-coil structure. It can be expressed in the seeds of
 CC transformed plants, e.g. soybean and corn, to increase lysine content

XX Sequence 28 AA;

Query Match 26.3%; Score 36; DB 2; Length 28;

Best Local Similarity 24.0%; Pred. No. 1.1e+03;

Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQETAA 25

DB 4 KMKAMEKMKAMEKMKAMEKMKKA 28

RESULT 42

AAW62935

ID AAW62935 standard; peptide; 28 AA.

XX AC AAW62935;

XX 02-OCT-1998 (first entry)

XX Minimalist lytic peptide.

XX Lytic peptide; channel forming peptide; antibacterial; amphipathic.

XX Synthetic.

XX US5789542-A.

XX 04-AUG-1998.
 XX 06-OCT-1997; 97US-00944133.
 XX 22-APR-1994; 94US-00232525.
 PR 22-JUL-1996; 96US-00681075.
 XX 03-FEB-1997; 97US-00789077.
 XX (LOUJ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.

XX Becker CL, McLaughlin ML;

XX WPI; 1998-446183/38.

XX Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-
 PT mer lytic peptides.

XX Disclosure; Col 5; 25pp; English.

XX AAW62920-67 represent minimalist lytic (channel forming) peptides. The
 CC peptides have antibacterial properties in concentrations not lethal
 CC toward mammalian cells. The peptides are heptads (or heptad multimers)
 CC that comprise four nonpolar amino acid residues and three positively
 CC charged amino acid residues, or five nonpolar amino acid residues and two
 CC positively charged amino acid residues. The nonpolar amino acid residues
 CC and the positively charged amino acid residues are distributed within the
 CC heptad such that when the multimer forms an alpha-helix the nonpolar
 CC amino acid residues will lie on one face of the alpha-helix, and the
 CC positively charged amino acid residues will lie on the opposite face of
 CC the alpha -helix, whereby the multimer is amphipathic

XX Sequence 28 AA;

Query Match 26.3%; Score 36; DB 2; Length 28;

Best Local Similarity 34.6%; Pred. No. 1.1e+03;

Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 IRALKWNAHLKQETAALEQETAALE 27

DB 3 LRALKKALKALKALKALKALKALK 28

RESULT 43

AAW60508

ID AAW60508 standard; protein; 28 AA.

XX AC AAW60508;

XX 25-MAR-2003 (revised)

DT 25-AUG-1998 (first entry)

XX Synthetic storage protein of the specification.

XX Dihydrodipicolinic acid synthase; DHPS; chimeric gene; storage protein;
 KW lysine inhibition; plant chloroplast transit sequence;
 KW plant seed-specific regulatory sequence; transgenic plant;
 KW increased lysine level; corn; Zea mays; soybean; Glycine max.

XX Synthetic.

XX US5773691-A.

XX 30-JUN-1998.

XX 07-JUN-1995; 95US-00474633.

XX 19-MAR-1992; 92US-00855414.

PR 18-MAR-1993; 93WO-US002480.

PR 06-JAN-1994; 94US-00178212.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

CC	insensitive to inhibition by lysine operably linked to a plant
CC	chloroplast transit sequence and to a plant seed-specific regulatory
CC	sequence. The chimeric genes are useful for producing plants containing
CC	increased levels of lysine, especially in corn (Zea mays) and soybean
CC	(Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
XX	
SQ	Sequence 28 AA;
	Query Match 26.3%; Score 36; DB 2; Length 28;
	Best Local Similarity 24.0%; Pred. No. 1.1e+03;
	Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
Qy	1 KIRALKWNHNLKQETIAALQETIAA 25
Db	4 KTKAMEEKMKAMEEKMKAMEEKMA 28

Search completed: November 21, 2005, 21:40:24
Job time : 131 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:36:04 ; Search time 23.5 Seconds
(without alignments)

114.641 Million cell updates/sec

Title: US-10-088-417a-4

Perfect score: 137

Sequence: 1 KIRALKWNAHLKQETAALEQETAALEQ 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 199

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	16.8	28	T38041	similarity to yeas
2	23	16.8	28	H85908	hypothetical prote
3	22	16.1	28	T47196	RAS protein [impor
4	21	15.3	28	S51067	ribosomal protein
5	21	15.3	28	A56499	brevicin-27 - Lact
6	21	15.3	28	T09594	gene LFV protein -
7	21	15.3	28	A44877	cell surface prote
8	20	14.6	28	I55596	lysosomal acid lip
9	20	14.6	28	S15235	hypothetical prote
10	20	14.6	28	S68643	nicotinic acetylch
11	20	14.6	28	C83969	hypothetical prote
12	19.5	14.2	28	S72460	ribosomal protein
13	19	13.9	28	I59477	antigen, T-cell re
14	19	13.9	28	S16228	aryl acylamidase -
15	19	13.9	28	P00625	homeobox JRX prote
16	19	13.9	28	I68614	frame shifted FMR1
17	18	13.1	28	J70412	bombyxin-IV chain
18	18	13.1	28	A03356	omega-glialdin - ei
19	18	13.1	28	S49924	stp protein (Baker
20	18	13.1	28	S64701	hypothetical prote
21	18	13.1	28	I39288	ZF3 domain - human
22	18	13.1	28	S70894	hypothetical prote
23	18	13.1	28	PC4430	peroxisome prolif
24	18	13.1	28	PC4429	peroxisome prolif
25	17.5	12.8	28	A61113	cellular retinol-b
26	17	12.4	28	1FSEW	trp operon leader
27	17	12.4	28	T14210	NADH2 dehydrogenas
28	17	12.4	28	S21278	glutathione transf
29	17	12.4	28	S39524	trRNA N-glycosidase

30	16	11.7	28	1	G9BPSV	gene 9 protein - s
31	16	11.7	28	2	A38296	sterol esterase (E
32	16	11.7	28	2	A60291	24K proteinase (EC
33	16	11.7	28	2	A32643	deoxyribodipyrimid
34	16	11.7	28	2	A61322	somatostatin-28 -
35	16	11.7	28	2	S21231	calcium-binding pr
36	16	11.7	28	2	I45911	dnak-type molecula
37	16	11.7	28	2	B54127	dolichyl-diphospho
38	16	11.7	28	2	T06340	ribosomal protein
39	15	10.9	28	2	S66436	allophycocyanin al
40	15	10.9	28	2	D38578	protein kinase 4 (
41	15	10.9	28	2	A35115	hypothetical prote
42	15	10.9	28	2	S07156	trypsin inhibitor
43	15	10.9	28	2	A27261	proteinase inhibit
44	15	10.9	28	2	PL0005	pepsin A (EC 3.4.2
45	15	10.9	28	2	PC2239	heat shock protein

ALIGNMENTS

RESULT 1

T38041

similarity to yeast mating protein SSF1 - fission yeast (Schizosaccharomyces pombe) (fra
C;Species: Schizosaccharomyces pombe
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
C;Accession: T38041
R;McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21764

A;Accession: T38041

A;Status: preliminary; translated from GE/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-28 <MCD>

A;Cross-references: UNIPARC:UPI0000162058; ENBL:AL109951; PIDN: CAB53054.1; GSPDB: GN00066

A;Experimental source: strain 972h-; cosmid c1B9

C;Genetics:

A;Gene: SPDB:SPAC1B9.01c

A;Map position: 1

Query Match 16.8%; Score 23; DB 2; Length 28;

Best Local Similarity 50.0%; Pred. No. 9.3e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 KNAHLKQES 15

Db 11 KRTHLKAD 18

RESULT 2

H85908

hypothetical protein Z3917 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85908
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85908

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <STO>

A;Cross-references: UNIPROT:Q8X415; UNIPARC:UPI000000D0867; GB:AE005174; NID:gl2517049; P
A;Experimental source: strain O157:H7, substrain EDU933
C;Genetics:

A;Gene: Z3917

Query Match 16.8%; Score 23; DB 2; Length 28;

Best Local Similarity 50.0%; Pred. No. 9.3e+03;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 18 ALQOEIAALE 27
| | : | |
Db 18 ATEETSLE 27

RESULT 3
T47196
RAS protein [imported] - Neurospora crassa (fragment)
C;Species: Neurospora crassa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47196
R;Lee, C.W.; Lee, E.
submitted to the EMBL Data Library, August 1995
A;Description: Structural analysis of ras genes from filamentous fungi.
A;Reference number: Z24384
A;Accession: T47196
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-28 <LEE>
A;Cross-references: UNIPROT:P22126; UNIPARC:UPI000016891F; EMBL:U33746; FIDN:AAA74986.1
C;Genetics:
A;Gene: ras
A;Note: Intron positions not resolved (incomplete sequence)
C;Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 1.3e+04;
Matches 5; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

QY 9 NAHLKQEIALEQEIHALE 27
::: ||| :| :| :|
Db 1 DSYRKQ--CTIDNEVALLD 17

RESULT 4
S51067
ribosomal protein S16 - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Date: 15-Jul-1995 #sequence_revision 01-Nov-1996 #text_change 01-Nov-1996
C;Accession: S51067
R;Tsiboli, P.; Herfurth, E.; Choli, T.
Eur. J. Biochem. 226, 169-177, 1994
A;Title: Purification and characterization of the 30S ribosomal proteins from the bacter
A;Reference number: S51053; MUID:95045586; PMID:7957245
A;Accession: S51067
A;Molecule type: protein
A;Residues: 1-28 <TSI>
A;Cross-references: UNIPARC:UPI00001772B2
A;Note: the source is designated as Thermus thermophilus
C;Superfamily: Escherichia coli ribosomal protein S16
C;Keywords: protein biosynthesis; ribosome

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 1.7e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KIRALKWKNAH 11
||| :| :|
Db 3 KIRLAREGSKH 13

RESULT 5
A56499
brevicin-27 - Lactobacillus brevis (strain SB27) (fragment)
C;Species: Lactobacillus brevis
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: A56499
R;Benoit, V.; Lebrini, A.; Humbert, G.; Lefebvre, G.
submitted to the Protein Sequence Database, June 1995
A;Description: Partial amino acid sequence of brevicin27, a bacteriocin which shares no
A;Reference number: A56499
A;Accession: A56499
A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-28 <LEB>
A;Cross-references: UNIPARC:UPI000017AD13

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ALKWKNA 10
| | | |
Db 8 AXTWGNA 14

RESULT 6
T09594
gene LFY protein - Monterey pine (fragment)
C;Species: Pinus radiata (Monterey pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09594
R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.
submitted to the EMBL Data Library, August 1996
A;Description: Partial characterization of Pinus radiata meristem identity homolog gene
A;Reference number: Z16756
A;Accession: T09594
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-28 <IZQ>
A;Cross-references: UNIPROT:O24285; UNIPARC:UPI00000AC880; EMBL:U66725; NTD:g1513305; PII
C;Genetics:
A;Gene: LFY
C;Function:
A;Description: controls meristem identity

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 22.2%; Pred. No. 1.7e+04;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIRALKWKNN 9
::: | :|
Db 19 RLKGRAWN 27

RESULT 7
A44877
cell surface protein 2F5 91K component - tobacco hornworm (fragment)
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44877
R;Nardi, J.B.
Dev. Biol. 152, 161-171, 1992
A;Title: Dynamic expression of a cell surface protein during rearrangement of epithelial
A;Reference number: A44877; MUID:92331807; PMID:1628754
A;Accession: A44877
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <NAR>
A;Cross-references: UNIPROT:Q9TWX0; UNIPARC:UPI000007FF81
A;Note: sequence extracted from NCBI backbone (NCBIP:108784)

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 27.8%; Pred. No. 1.7e+04;
Matches 5; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 7 WKNA----HLKOEIAALE 20
| :| :| :| :|
Db 5 WRVADSELSLEVKQIESFE 22

RESULT 8
I55596
lysosomal acid lipase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C;Accession: I55596
R;Klima, H.; Ullrich, K.; Aelaniadis, C.; Fehring, P.; Lackner, K.J.; Schmitz, G.
J. Clin. Invest. 92, 2713-2718, 1993
A;Title: A splice junction mutation causes deletion of a 72-base exon from the mRNA for
A;Reference number: I55596; MUID:94075617; PMID:8254026
A;Accession: I55596
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-28 <RES>
A;Cross-references: UNIPARC:UPI000011F7AC; GB:S68069; NID:G544574; PIDN:AAB29185.1; PID:
C;Superfamily: triacylglycerol lipase, lingual

Query Match 14.6%; Score 20; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 2.3e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIRALKW 7
Db 21 KFOAFDW 27

RESULT 9
S15235
hypothetical protein - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S15235
R;Perry, A.C.F.; Bhriain, N.N.; Brown, N.L.; Rouch, D.A.
Mol. Microbiol. 5, 163-171, 1991
A;Title: Molecular characterization of the gor gene encoding glutathione reductase from
ses.
A;Reference number: S15235; MUID:91194546; PMID:1849605
A;Accession: S15235
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <PER>
A;Cross-references: UNIPROT:P23205; UNIPARC:UPI000016FCAP; EMBL:X54201; NID:G45324; PIDN:

Query Match 14.6%; Score 20; DB 2; Length 28;
Best Local Similarity 35.3%; Pred. No. 2.3e+04;
Matches 6; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 11 HLKQEIHALEQEIHALE 27
Db 7 HLALHVPDLDCIAPYE 23

RESULT 10
S68643
nicotinic acetylcholine receptor-binding protein 3C - black-banded coral snake (fragment)
C;Species: Micrurus nigrocinctus (black-banded coral snake)
C;Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S68643
R;Alape-Giron, A.; Stiles, B.; Schmidt, J.; Giron-Cortes, M.; Thelestam, M.; Joernvall,
FEBS Lett. 380, 29-32, 1996
A;Title: Characterization of multiple nicotinic acetylcholine receptor-binding proteins
A;Reference number: S68639; MUID:96181662; PMID:8603741
A;Accession: S68643
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <ALA>
A;Cross-references: UNIPROT:Q9PRQ3; UNIPARC:UPI00000FDC7B

Query Match 14.6%; Score 20; DB 2; Length 28;
Best Local Similarity 57.1%; Pred. No. 2.3e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIRALKW 7
Db 22 KIXPKKW 28

RESULT 11

C83969
hypothetical protein BH2555 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83969
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <STO>
A;Cross-references: UNIPROT:Q9K9U0; UNIPARC:UPI00000C3F36; GB:AF001515; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2555

Query Match 14.6%; Score 20; DB 2; Length 28;
Best Local Similarity 30.0%; Pred. No. 2.3e+04;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 KWKNAHLKQE 15
Db 12 KLNRVHISQ 21

RESULT 12
S72460
ribosomal protein S19 - curled-leaved tobacco chloroplast (fragment)
C;Species: Chloroplast Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S72460
R;Goulding, S.E.; Olmstead, R.G.; Morden, C.W.; Wolfe, K.H.
Mol. Gen. Genet. 252, 195-206, 1996
A;Title: Ebb and flow of the chloroplast inverted repeat.
A;Reference number: S72459; MUID:96397499; PMID:8804393
A;Accession: S72460
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <GOU>
A;Cross-references: UNIPROT:Q36593; UNIPARC:UPI000008D033; EMBL:Z71241; NID:G1279593; PI
A;Note: only a part of the nucleic acid sequence is shown
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
C;Genetics:
A;Gene: rps19
A;Genome: chloroplast
A;Start codon: GTG
C;Function:
A;Pathway: protein biosynthesis
C;Superfamily: ribosomal protein S19/S15
C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 14.2%; Score 19.5; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 2.6e+04;
Matches 9; Conservative 3; Mismatches 4; Indels 5; Gaps 2;

Qy 3 RALKWQNA----HLKQEIHALE 19
Db 3 RSLK-KNPFVANHLKKIDKL 22

RESULT 13
I59477
antigen, T-cell receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I59477
R;Mathioudakis, G.; Chen, P.
Scand. J. Immunol. 38, 31-36, 1993
A;Title: Preferential rearrangements of the V gamma 1 subgroup of the gamma-chain of the
Tmal donors.
A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-28 <RES>
A;Cross-references: UNIPARC:UPI0000117281; GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:
C;Keywords: T-cell receptor

Query Match 13.9%; Score 19; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 3.1e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 WKNAHLKQ 14
| | | | |
Db 4 WDPATYKK 11
| | | | |

RESULT 14
S16228
aryl acylamidase - Nocardia globnerula
C;Species: Nocardia globnerula
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S16228
R;Yoshioka, H.; Nagasawa, T.; Yamada, H.
Eur. J. Biochem. 199, 17-24, 1991
A;Title: Purification and characterization of aryl acylamidase from Nocardia globnerula.
A;Reference number: S16228; MUID:91293120; PMID:2065673
A;Accession: S16228
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <EUR>
A;Cross-references: UNIPROT:P80008; UNIPARC:UPI00001260D8

Query Match 13.9%; Score 19; DB 2; Length 28;
Best Local Similarity 35.0%; Pred. No. 3.1e+04;
Matches 7; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 10 AHLKQEIATL--RQETAALE 27
| | | | | : | | | | |
Db 8 AHDTGLAELIREGQVSACE 27
| | | | | : | | | | |

RESULT 15
PN0625
homeobox JRX protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 05-Oct-2004
C;Accession: PN0625
R;Inamori, K.; Takeashita, K.; Chiba, S.; Yazaki, Y.; Hirai, H.
Biochem. Biophys. Res. Commun. 195, 203-208, 1993
A;Title: Identification of homeobox genes expressed in human T-lymphocytes.
A;Reference number: PN0625; MUID:94029995; PMID:8105782
A;Accession: PN0625
A;Molecule type: DNA
A;Residues: 1-28 <INA>
A;Cross-references: UNIPROT:Q9UD92; UNIPARC:UPI000006F5FA
A;Experimental source: T-lymphocyte
C;Comment: This protein is the product of the divergent classes of homeobox gene and par
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 13.9%; Score 19; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 3.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 KQEIATL 18
| | | | |
Db 12 KAEIAA 17
| | | | |

RESULT 16
I68614
frame shifted FMR1 exon - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C;Accession: I68614; I68615
R;Eichler, E.E.; Richards, S.; Gibbs, R.A.; Nelson, D.L.
Hum. Mol. Genet. 2, 1147-1153, 1993
A;Title: Fine structure of the human FMR1 gene.
A;Reference number: I54334; MUID:94004853; PMID:8401496
A;Accession: I68614
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <EII>
A;Cross-references: UNIPROT:Q16578; UNIPARC:UPI000006DBIC; GB:L19490; NID:g388747; PIDN:
A;Accession: I68615
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <EII2>
A;Cross-references: UNIPARC:UPI000006DBIC; GB:L19491; NID:g388749; PIDN:AAA62467.1; PID:
C;Comment: This sequence appears to be the frame shifted hypothetical translation of an e
C;Genetics:
A;Gene: GDB:FMR1
A;Cross-references: GDB:129038; OMIM:309550
A;Map position: Xq27.3-Xq27.3

Query Match 13.9%; Score 19; DB 4; Length 28;
Best Local Similarity 37.5%; Pred. No. 3.1e+04;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 11 HLKQEIATLEQEIATL 26
| | | | | : | | | | |
Db 12 HVIQERLKEQRKTCL 27
| | | | | : | | | | |

RESULT 17
JT0412
bombyxin-IV chain B - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998
C;Accession: JT0412
R;Maruyama, K.; Hietter, H.; Nagasawa, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki,
Agric. Biol. Chem. 52, 3035-3041, 1988
A;Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of bon
A;Reference number: JT0410
A;Accession: JT0412
A;Molecule type: protein
A;Residues: 1-28 <MAR>
A;Cross-references: UNIPARC:UPI000017665E
C;Superfamily: insulin
C;Keywords: pyroglutamic acid
F;10/Modified site: pyroglutamic acid (Gln) #status experimental
F;10/Disulfide bonds: interchain (to chain A-7) #status predicted
F;22/Disulfide bonds: interchain (to chain A-20) #status predicted

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 44.4%; Pred. No. 4.1e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 HLKQEIATL 19
| | | | | : | | | | |
Db 13 HLANTLADL 21
| | | | | : | | | | |

RESULT 18
A03356
omega-gliadin - einkorn wheat (fragment)
C;Species: Triticum monococcum (einkorn wheat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A03356
R;Shewry, P.R.; Autran, J.C.; Nimmo, C.C.; Lew, E.J.L.; Kasarda, D.D.
Nature 286, 520-522, 1980
A;Reference number: A93228
A;Accession: A03356
A;Molecule type: protein
A;Residues: 1-28 <SHE>
A;Cross-references: UNIPROT:P02865; UNIPARC:UPI000012B3AA
C;Superfamily: gliadin

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 4.1e+04;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 20 EQEIAALEQ 28
:|:|:|:|:|:|
Db 8 DQELQSPQQ 16

RESULT 19
S49924
stp protein (Baker variant) - phage OX2
C;Species: phage OX2
C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55803; S49924
R;Penner, M.; Morad, I.; Snyder, L.; Kaufmann, G.
J. Mol. Biol. 249, 857-868, 1995
A;Title: Phage T4-coded Stp: double-edged effector of coupled DNA and tRNA-restriction
A;Reference number: S55796; MUID:95311310; PMID:7791212
A;Accession: S55803
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-28 <PEN>
A;Cross-references: UNIPROT:Q38060; UNIPARC:UPI000009C058; EMBL:Z46880; NID:G599663; PID
C;Genetics:
A;Gene: stp
C;Superfamily: phage T4 stp protein

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.1e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 NAHLKQ 14
:|:|:|
Db 6 NEHVMQ 11

RESULT 20
S64701
hypothetical protein (aph1 5'-region) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S64701
R;Huang, Y.; Garrison, P.N.; Barnes, L.D.
Biochem. J. 312, 925-932, 1995
A;Title: Cloning of the Schizosaccharomyces pombe gene encoding diadenosine 5',5'-P(1)
n family.
A;Reference number: S64700; MUID:96128081; PMID:8554540
A;Accession: S64701
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <HUA>
A;Cross-references: UNIPARC:UPI000017B1D8; EMBL:U32615

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 23.1%; Pred. No. 4.1e+04;
Matches 3; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 8 KNAHLKQEIAALE 20
:|:|:|:|:|:|
Db 14 REAEFNQQLRFLQ 26

RESULT 21
I39288
ZF3 domain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I39288
R;Ogawa, O.; Eccles, M.R.; Yun, K.; Mueller, R.F.; Holdaway, M.D.; Reeve, A.E.
Hum Mol Genet. 2, 203-204, 1993
A;Title: A novel insertional mutation at the third zinc finger coding region of the WT1

A;Reference number: I39288; MUID:93271969; PMID:8098976
A;Accession: I39288
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <RES>
A;Cross-references: UNIPARC:UPI00000006BE; EMBL:X72314; NID:G312849; PIDN:CAA51057.1; PFI
C;Genetics:
A;Gene: GDB:WT1
A;Cross-references: GDB:120496; OMIM:194070
A;Map position: 11p13-11p13

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KNAHLK 13
:|:|:|
Db 11 RSDHLK 16

RESULT 22
S70894
hypothetical protein 1 - Vibrio anguillarum (fragment)
C;Species: Vibrio anguillarum
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S70894
R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.
Mol. Microbiol. 19, 625-637, 1996
A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen
A;Reference number: S70894; MUID:96228710; PMID:8830252
A;Accession: S70894
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <OTO>
A;Cross-references: UNIPROT:Q92883; UNIPARC:UPI000000BD25A; GB:U36378; EMBL:L47344; NID:G

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 4.1e+04;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 KWKNAH 11
:|:|
Db 10 EWQVTH 15

RESULT 23
PC4430
peroxisome proliferator activated receptor gamma variant, P12A - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C;Accession: PC4430
R;Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K.
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A;Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
A;Reference number: PC4429; MUID:98086341; PMID:9425261
A;Accession: PC4430
A;Molecule type: DNA
A;Residues: 1-28 <YEN>
A;Cross-references: UNIPARC:UPI000017ALD0
C;Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
C;Genetics:
A;Introns: 28/1

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 4.1e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 NAHLKQE 15
:|:|:|
Db 22 SANISQE 28

RESULT 24

PC4429
peroxisome proliferator activated receptor gamma - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C;Accession: PC4429
R;Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K.
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A;Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
A;Reference number: PC4429; MUID:98086341; PMID:9425261
A;Accession: PC4429
A;Molecule type: DNA
A;Residues: 1-28 <YEN>
A;Cross-references: UNIPARC:UPI000017A1CF
C;Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
C;Genetics:
A;Introns: 28/1

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 4.1e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 NAHLKQE 15
|:|:|
DB 22 SANISQE 28

RESULT 25
A61113
cellular retinol-binding protein II - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: A61113
R;Finlay, J.A.; Deluca, H.F.
Biochemistry 27, 3381-3387, 1988
A;Title: Purification and properties of an 18-kilodalton, 1,25-dihydroxyvitamin D-3 modu
A;Reference number: A61113; MUID:88269534; PMID:3390438
A;Accession: A61113
A;Molecule type: protein
A;Residues: 1-28 <FIN>
A;Cross-references: UNIPROT:Q7LZ76; UNIPARC:UPI0000177825
C;Superfamily: myelin P2 protein

Query Match 12.8%; Score 17.5; DB 2; Length 28;
Best Local Similarity 23.8%; Pred. No. 4.7e+04;
Matches 5; Conservative 6; Mismatches 7; Indels 3; Gaps 1;

QY 7 WK---NAHLKQEIALEQEIFA 24
|:|:|:|:|:|
DB 8 WEMESNFEQYVADIDFA 28

RESULT 26
LFSEW
trp operon leader peptide - Serratia marcescens
C;Species: Serratia marcescens
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C;Accession: A03591
R;Miozzari, G.F.; Yanofsky, C.
Nature 276, 684-689, 1978
A;Title: The regulatory region of the trp operon of Serratia marcescens.
A;Reference number: A93202; MUID:7903989; PMID:366432
A;Accession: A03591
A;Molecule type: DNA
A;Residues: 1-28 <MIO>
A;Cross-references: UNIPROT:P03055; UNIPARC:UPI000012E89F
C;Genetics:
A;Gene: trpL
C;Function:
A;Description: Involved in control of tryptophan operon transcription by attenuation
C;Superfamily: trp leader peptide

Query Match 12.4%; Score 17; DB 1; Length 28;
Best Local Similarity 28.6%; Pred. No. 5.4e+04;

Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 WKNAHLK 13
|:|:|
DB 20 WRTSLLR 26

RESULT 27
T14210
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Uromastyx acanthinurus mitochondr
C;Species: mitochondrion Uromastyx acanthinurus
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14210
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
A;Reference number: Z17789; MUID:97153826; PMID:9000757
A;Accession: T14210
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <MAC>
A;Cross-references: UNIPROT:P92760; UNIPARC:UPI0000099123; EMBL:U71325; NID:g1753264; PFI
A;Experimental source: specimen voucher MV2162567; Museum of Vertebrate Zoology, Universi
C;Genetics:
A;Genome: mitochondrion
A;Note: NDI
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 12.4%; Score 17; DB 2; Length 28;
Best Local Similarity 44.4%; Pred. No. 5.4e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 HLKQEIATAAL 19
|:|:|:|
DB 15 NLPSALAAAL 23

RESULT 28
S21278
glutathione transferase (EC 2.5.1.18) alpha-Yx - rat (fragment)
N;Alternate names: glutathione S-transferase Yx; glutathione transferase Yfetus
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: S21278
R;Igataashi, T.; Tsuchiya, T.; Shikata, Y.; Sagami, F.; Tagaya, O.; Horie, T.; Satoh, T.
Biochem. J. 283, 307-311, 1992
A;Title: Developmental aspects of a unique glutathione S-transferase subunit Yx in the l
Yfetus.
A;Reference number: S21278; MUID:92231842; PMID:1567376
A;Accession: S21278
A;Molecule type: protein
A;Residues: 1-28 <IGA>
A;Cross-references: UNIPROT:Q9JLQ6; UNIPARC:UPI00000E725F
C;Superfamily: glutathione transferase
C;Keywords: dimer; liver; transferase

Query Match 12.4%; Score 17; DB 2; Length 28;
Best Local Similarity 14.3%; Pred. No. 5.4e+04;
Matches 1; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIRALKW 7
|:|:|
DB 14 RMEPIRW 20

RESULT 29
S38524
rRNA N-glycosidase (EC 3.2.2.22) saporin R1 - common soapwort (fragment)
C;Species: Saponaria officinalis (common soapwort)
C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S38524
R;Ferreira, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; Rojo


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Biochim. Biophys. Acta 1216, 31-42, 1993
A;Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA
A;Reference number: S38521; MUID:94032486; PMID:8218413
A;Accession: S38524
A;Molecule type: protein
A;Residues: 1-28 <FER>
A;Cross-references: UNIPROT:Q7MLI8; UNIPARC:UPI0000017AF39
C;Keywords: glycosidase; hydrolase

Query Match      12.4%; Score 17; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 5.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      5 LKW 7
      :||
Db      4 VKW 6

RESULT 30
G9BRSV
Gene 9 protein - spiroplasma virus 4
C;Species: spiroplasma virus 4, SpV4
A;Note: host Spiroplasma melliferum
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B29825
R;Renaudin, J.; Pascarel, M.C.; Bove, J.M.
J. Bacteriol. 169, 4950-4961, 1987
A;Title: Spiroplasma virus 4: nucleotide sequence of the viral DNA, regulatory signals,
A;Reference number: A91845; MUID:88032809; PMID:2822658
A;Accession: B29825
A;Molecule type: DNA
A;Residues: 1-28 <REN>
A;Cross-references: UNIPROT:P11341; UNIPARC:UPI0000013863B; GB:M17988; MID:G334998
A;Note: This ORF is not annotated in GenBank entry SPVDNA
C;Comment: This virus is a procaryote DNA virus.
C;Genetics:
A;Gene: 9
A;Genetic code: SGC3
A;Superfamily: spiroplasma virus 4 gene 9 protein

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.1e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      6 KWKN 9
      :||
Db      19 RWFN 22

RESULT 31
A38296
sterol esterase (EC 3.1.1.13) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 14-Nov-1997
C;Accession: A38296
R;DiPersio, L.P.; Pontaine, R.N.; Hui, D.Y.
J. Biol. Chem. 265, 16801-16806, 1990
A;Title: Identification of the active site serine in pancreatic cholesterol esterase by
A;Reference number: A38296; MUID:91009095; PMID:2211595
A;Accession: A38296
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DIP>
A;Cross-references: UNIPARC:UPI00000175911
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein

Query Match      11.7%; Score 16; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.1e+04;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      16 IAALEQEIATA 25
      || : |||

```

Db 2 IALVITNIAA 11

RESULT 32

A60291

24K proteinase (EC 3.4.-.-) - silkworm (fragment)

C;Species: Bombyx mori (silkworm)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 15-Oct-1999

C;Accession: A60291

R;Ikeda, M.; Sasaki, T.; Yamashita, O.

Insect Biochem. 20, 725-734, 1990

A;Title: Purification and characterization of proteases responsible for vitellin degradation

A;Reference number: A60291

A;Accession: A60291

A;Molecule type: protein

A;Residues: 1-28 <IRE>

A;Cross-references: UNIPARC:UPI00000175C3C

C;Comment: This enzyme degrades the nutritional yolk protein vitellin during embryogenesis

C;Superfamily: trypsin; trypsin homology

C;Keywords: egg yolk; hydrolase

Query Match 11.7%; Score 16; DB 2; Length 28;

Best Local Similarity 40.0%; Pred. No. 7.1e+04;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 17 AALEQEIAAL 26

Db 19 ASMXNIAAL 28

RESULT 33

A32643

deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Methanobacterium thermoautotrophicum

N;Alternate names: photoreactivating enzyme

C;Species: Methanobacterium thermoautotrophicum

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Apr-1999

C;Accession: A32643

R;Kiener, A.; Husein, I.; Sancar, A.; Walsh, C.

J. Biol. Chem. 264, 13880-13887, 1989

A;Title: Purification and properties of Methanobacterium thermoautotrophicum DNA photolyase

A;Reference number: A32643; MUID:89340481; PMID:2668276

A;Accession: A32643

A;Molecule type: protein

A;Residues: 1-28 <KIE>

A;Cross-references: UNIPARC:UPI000001319F6

C;Superfamily: deoxyribodipyrimidine photo-lyase

C;Keywords: carbon-carbon lyase; DNA binding

Query Match 11.7%; Score 16; DB 2; Length 28;

Best Local Similarity 60.0%; Pred. No. 7.1e+04;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIRAL 5

Db 6 RIRSL 10

RESULT 34

A61322

somatostatin-28 - sheep

N;Contains: somatostatin-14

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C;Accession: A61322; A61344

R;Spiess, J.; Villarreal, J.; Vale, W.

Biochemistry 20, 1982-1988, 1981

A;Title: Isolation and sequence analysis of a somatostatin-like polypeptide from ovine

A;Reference number: A61322; MUID:81184502; PMID:7225368

A;Accession: A61322

A;Molecule type: protein

A;Residues: 1-28 <SPI>

A;Cross-references: UNIPARC:UPI000002F1CD

R;Burgus, R.; Ling, N.; Butcher, M.; Guillemin, R.

Proc. Natl. Acad. Sci. U.S.A. 70, 684-688, 1973
 A:Title: Primary structure of somatostatin, a hypothalamic peptide that inhibits the secretion of growth hormone releasing hormone
 A:Reference number: A61344; MUID:73209562; PMID:4514982
 A:Accession: A61344
 A:Molecule type: protein
 A:Residues: 15-28 <EUR>
 A:CROSS-references: UNIPARC:UPI000002BB13
 C:Superfamily: somatostatin
 C:Keywords: neuropeptide
 F:1-28/Product: somatostatin-28 #status experimental <S28>
 F:15-28/Product: somatostatin-14 #status experimental <S14>
 F:17-28/Disulfide bonds: #status experimental

Query Match 11.7%; Score 16; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WK 8
 ||
 DB 22 WK 23

RESULT 35
 S21231
 calcium-binding protein SCP VI, sarcoplasmic - common lancelet
 C:Species: Branchiostoma lanceolatum (common lancelet)
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002
 C:Accession: S21231
 R:Tagaki, T.; Valette-Talbi, L.; Cox, J.A.
 FEBS Lett. 302, 159-160, 1992
 A:Title: Primary structure of three minor isoforms of amphioxus sarcoplasmic calcium-binding protein
 A:Reference number: S21153; MUID:92339504; PMID:1633848
 A:Accession: S21231
 A:Molecule type: protein
 A:Residues: 1-28 <TAK>
 A:CROSS-references: UNIPARC:UPI0000177710
 C:Superfamily: calmodulin; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand

Query Match 11.7%; Score 16; DB 2; Length 28;
 Best Local Similarity 16.7%; Pred. No. 7.1e+04;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 ALKWN 9
 ::::
 DB 14 SIQWMD 19

RESULT 36
 I45911
 dnaK-type molecular chaperone hsp70A - bovine (fragment)
 N:Alternate names: heat shock protein
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Dec-2004
 C:Accession: I45911
 R:Kowalski, J.; Gilbert, S.A.; van Drunen-Littel-van den Hurk, J.; Bab
 Vaccine 11, 1100-1107, 1993
 A:Title: Heat-Shock Promoter-Driven Synthesis of Secreted Herpesvirus Glycoproteins in T
 A:Reference number: I45911; MUID:94070117; PMID:8249428
 A:Accession: I45911
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-28 <KOW>
 A:CROSS-references: UNIPROT:Q27965; UNIPARC:UPI000016C320; GB:M98823; NID:g409185; PIDN:
 C:Genetics:
 A:Gene: hsp70A
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein complex
 C:Superfamily: bcr protein
 C:Keywords: ATP; molecular chaperone

Query Match 11.7%; Score 16; DB 2; Length 28;
 Best Local Similarity 66.7%; Pred. No. 7.1e+04;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 HLKQEI 16
 ||||
 DB 23 HGKVEI 28

RESULT 37
 B54127
 dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) 65k chain I - c
 N:Alternate names: oligosaccharyltransferase
 C:Species: Gallus gallus (chicken)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
 C:Accession: B54127
 R:Kumar, V.; Heinemann, F.S.; Ozols, J.
 J. Biol. Chem. 269, 13451-13457, 1994
 A:Title: Purification and characterization of avian oligosaccharyltransferase. Complete
 A:Reference number: A54127; MUID:94230453; PMID:8175777
 A:Accession: B54127
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-28 <KUM>
 A:CROSS-references: UNIPROT:P80896; UNIPARC:UPI0000130EC4
 C:Superfamily: Caenorhabditis elegans hypothetical protein T22D1.4
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 11.7%; Score 16; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WK 8
 ||
 DB 22 WK 23

RESULT 38
 T06340
 ribosomal protein S16 - soybean chloroplast (fragment)
 C:Species: chloroplast Glycine max (soybean)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06340
 R:Nielsen, N.C.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: Z15613
 A:Accession: T06340
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-28 <NIE>
 A:CROSS-references: UNIPROT:Q32307; UNIPARC:UPI000008B5A1; EMBL:U26948; NID:g984307; PIDN:
 A:Experimental source: cultivar Resnik; leaf
 C:Genetics:
 A:Gene: rps16
 A:Genome: chloroplast
 C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 11.7%; Score 16; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KW 7
 ||
 DB 22 KW 23

RESULT 39
 S66436
 allophycocyanin alpha-B chain - Anabaena sp. (strain PCC 7120) (fragment)
 C:Species: Anabaena sp.
 A:Variety: PCC 7120
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S66436
 R:Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.
 Eur. J. Biochem. 236, 1010-1024, 1996

A;Title: Isolation, characterization and electron microscopy analysis of a hemidiscoideum
A;Reference number: S66435; MUID:96270757; PMID:8665889
A;Accession: S66436
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DUC>
A;Cross-references: UNIPROT:P80556; UNIPARC:UPI00000174E0E
C;Superfamily: phycocyanin

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 9.1e+04;
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LKQEIALLQEQL 23
: : : :
Db 3 ISQVILQADDEL 14

RESULT 40
A27578
protein kinase 4 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 23-Feb-1997
C;Accession: D38578
R;Haribabu, B.; Dettin, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum
A;Reference number: A38578; MUID:91142122; PMID:1996312
A;Accession: D38578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPARC:UPI000017556D; GB:M59747
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 9.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HLK 13
: :
Db 8 HIK 10

RESULT 41
A35115
hypothetical protein (trpG 5' region) - Pseudomonas putida
C;Species: Pseudomonas putida
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: A35115
R;Essar, D.W.; Eberly, L.; Crawford, I.P.
J. Bacteriol. 172, 867-883, 1990
A;Title: Evolutionary differences in chromosomal locations of four early genes of the trpGDC.
A;Reference number: A35115; MUID:90130325; PMID:2404959
A;Accession: A35115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <ESS>
A;Cross-references: UNIPROT:Q52275; UNIPARC:UPI00000837F8; GB:M33799; NID:9151627; PIDN:
C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 9.1e+04;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KWK 8
: :
Db 23 RWR 25

RESULT 42

A;Title: Isolation, characterization and electron microscopy analysis of a hemidiscoideum
A;Reference number: S66435; MUID:96270757; PMID:8665889
A;Accession: S66436
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DUC>
A;Cross-references: UNIPROT:P80556; UNIPARC:UPI00000174E0E
C;Superfamily: phycocyanin

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 9.1e+04;
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LKQEIALLQEQL 23
: : : :
Db 3 ISQVILQADDEL 14

RESULT 40
A27578
protein kinase 4 (EC 2.7.1.1) - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostelium discoideum
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 23-Feb-1997
C;Accession: D38578
R;Haribabu, B.; Dettin, R.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991
A;Title: Identification of a protein kinase multigene family of Dictyostelium discoideum
A;Reference number: A38578; MUID:91142122; PMID:1996312
A;Accession: D38578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPARC:UPI000017556D; GB:M59747
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 9.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HLK 13
: :
Db 8 HIK 10

RESULT 41
A35115
hypothetical protein (trpG 5' region) - Pseudomonas putida
C;Species: Pseudomonas putida
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: A35115
R;Essar, D.W.; Eberly, L.; Crawford, I.P.
J. Bacteriol. 172, 867-883, 1990
A;Title: Evolutionary differences in chromosomal locations of four early genes of the trpGDC.
A;Reference number: A35115; MUID:90130325; PMID:2404959
A;Accession: A35115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <ESS>
A;Cross-references: UNIPROT:Q52275; UNIPARC:UPI00000837F8; GB:M33799; NID:9151627; PIDN:
C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 9.1e+04;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KWK 8
: :
Db 23 RWR 25

RESULT 42

S07156
trypsin inhibitor III - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S07156
R;Nowak, K.; Słominska, A.; Polanowski, A.; Wiecezorek, M.; Wilusz, T.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1017-1019, 1981
A;Title: Trypsin inhibitor III from squash seeds (Cucurbita maxima), its reactive site a
A;Reference number: S07156; MUID:82005824; PMID:7275008
A;Accession: S07156
A;Molecule type: protein
A;Residues: 1-28 <NOW>
A;Cross-references: UNIPROT:P07853; UNIPARC:UPI00001763BE
C;Superfamily: squash trypsin inhibitor ITD I
C;Keywords: disulfide bond
F;3-21,10-25/Disulfide bonds: #status predicted
F;5/Inhibitory site: Arg (trypsin) #status experimental

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.1e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 15 EIAALE 20
: :
Db 19 EVCHLE 24

RESULT 43
A27261
proteinase inhibitor 3 - sea anemone (Stichodactyla sp.) (fragments)
C;Species: Stichodactyla sp.; Stichodactis sp.
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
C;Accession: A27261
R;Mebs, D.; Gebauer, E.
Toxicol. 20, 335, 1982
A;Title: Structural studies on a proteinase inhibitor from the sea anemone Stichodactis
A;Reference number: A27261
A;Accession: A27261
A;Molecule type: protein
A;Residues: 1-28 <MEB>
A;Cross-references: UNIPARC:UPI000017B685

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 20 EQEIAA 25
: :
Db 17 ERTLAA 22

RESULT 44
PL0005
pepsin A (EC 3.4.23.1) precursor - Mongolian sheep (fragments)
C;Species: Ovis platyura (Mongolian sheep)
C;Date: 30-Jun-1992 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
C;Accession: PL0005
R;Baudys, M.; Erdene, T.G.; Kostka, V.; Pavlik, M.; Foltmann, B.
Comp. Biochem. Physiol. B 89, 385-391, 1988
A;Title: Comparison between prochymosin and pepsinogen from lamb and calf.
A;Reference number: PL0006; MUID:88185059; PMID:3128424
A;Accession: PL0005
A;Molecule type: protein
A;Residues: 1-15;16-28 <BAU>
A;Cross-references: UNIPARC:UPI000017C5AD; UNIPARC:UPI000017C5AE
A;Experimental source: stomach
C;Keywords: aspartic proteinase; hydrolase; protein digestion; zymogen
F;1-15/Domain: activation peptide (fragment) #status predicted <ACP>

Query Match 10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 44.4%; Pred. No. 9.1e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIPALWKN 9
 || : || :
 Db 4 KIPLVKKS 12

RESULT 45

PC2239
 heat shock protein, high-molecular-mass 105B - mouse (fragments)
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
 C:Accession: PC2239
 R:Hatayama, T.; Yasuda, K.; Nishiyama, E.
 Biochem. Biophys. Res. Commun. 204, 357-365, 1994
 A:Title: Characterization of high-molecular-mass heat shock proteins and 42oC-specific h
 A:Reference number: PC2238; MUID:95032120; PMID:7945382
 A:Accession: PC2239
 A:Molecule type: protein
 A:Residues: 1-28 <HAT>
 A:Cross-references: UNIPARC:UPI000017C679
 C:Keywords: heat shock; stress-induced protein

Query Match 10.9%; Score 15; DB 2; Length 28;
 Best Local Similarity 40.0%; Pred. No. 9.1e+04;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 16 IAALE 20
 :|||
 Db 4 VSAIE 8

Search completed: November 21, 2005, 21:47:33
 Job time : 24.5 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:26:34 ; Search time 142 Seconds
(without alignments)
139.118 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWNAHLKQETALRQETAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1678

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	22.6	28	Q4SXA6_TETNG	Q4sxa6 tetraodon n
2	30	21.9	28	Q9IN95_GHIV1	Q9in95 human immun
3	29	21.2	28	Q4XP22_PLACH	Q4xp22 plasmodium
4	28	20.4	28	Q4TT22_9SPHN	Q4tt22 erythroblast
5	28	20.4	28	Q4RCL2_TETNG	Q4rcl2 tetraodon n
6	27	19.7	28	Q4YD65_PLABE	Q4yd65 plasmodium
7	27	19.7	28	Q4TIF5_TETNG	Q4tif5 tetraodon n
8	26	19.0	28	Q8ZYV3_PVRAB	Q8zyv3 pyrobaculum
9	26	19.0	28	Q7GHK5_AEDAL	Q7ghk5 aedes albop
10	26	19.0	28	Q4Z2J3_PLABE	Q4z2j3 plasmodium
11	26	19.0	28	Q6AGW8_LEIXX	Q6agw8 leifsonia x
12	25	18.2	28	Q9TWV5_PERAM	Q9twv5 periplaneta
13	25	18.2	28	Q4X6M9_PLACH	Q4x6m9 plasmodium
14	25	18.2	28	Q4XC88_PLACH	Q4xc88 plasmodium
15	24	17.5	28	Q6U7R1_CRYNV	Q6u7r1 cryptococcu
16	24	17.5	28	Q00440_GLOLA	Q00440 glomerella
17	24	17.5	28	Q2TW22_PARLI	Q2tw22 paracentrot
18	24	17.5	28	Q99LW3_MOUSE	Q99lw3 mus musculu
19	24	17.5	28	Q4T3N5_TETNG	Q4t3n5 tetraodon n
20	23	16.8	28	Q33TM9_HUMAN	Q33tm9 homo sapien
21	23	16.8	28	Q4XCS0_PLACH	Q4xcso plasmodium
22	23	16.8	28	Q4YAC7_PLACH	Q4yac7 plasmodium
23	23	16.8	28	Q94IS1_PINRA	Q94is1 pinus radia
24	23	16.8	28	Q4NC96_9WICC	Q4nc96 arthrobacte
25	23	16.8	28	Q8X415_ECO57	Q8x415 escherichia
26	23	16.8	28	Q91VP0_MOUSE	Q91vp0 mus musculu
27	22	16.1	28	Q7SI05_NEUCR	Q7si05 neurospora
28	22	16.1	28	P87021_MAGGR	P87021 magnaporthe
29	22	16.1	28	Q4Y377_PLACH	Q4y377 plasmodium
30	22	16.1	28	Q4YE24_PLABE	Q4ye24 plasmodium
31	22	16.1	28	Q4YQ82_PLABE	Q4yq82 plasmodium

32	22	16.1	28	2	Q4Z0C3_PLABE	Q4z0c3 plasmodium
33	22	16.1	28	2	O62731_CANFA	O62731 canis famil
34	22	16.1	28	2	O9GMF5_PAPHA	O9gmf5 papio hanad
35	22	16.1	28	2	O9GMF6_MACMU	O9gmf6 macaca mula
36	22	16.1	28	2	Q9XGE6_VICFA	Q9xge6 vicia faba
37	22	16.1	28	2	Q50102_MYCLE	Q50102 mycobacteri
38	22	16.1	28	2	Q93JY6_MYCTU	Q93jy6 mycobacteri
39	22	16.1	28	2	Q724A1_LISMF	Q724a1 listeria mo
40	22	16.1	28	2	Q4RFB7_TETNG	Q4rfb7 tetraodon n
41	22	16.1	28	2	Q4SVA3_TETNG	Q4sva3 tetraodon n
42	21.5	15.7	28	2	Q5F210_MOUSE	Q5f210 mus musculu
43	21	15.3	28	1	GRP_ALLEMI	P31886 alligator m
44	21	15.3	28	2	Q5AW44_EMENI	Q5aw44 aspergillus
45	21	15.3	28	2	Q9TWX0_MANSE	Q9twx0 manduca sex

ALIGNMENTS

RESULT 1

Q4SXA6_TETNG
ID Q4SXA6_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4SXA6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DB Chromosome undetermined SCAP12653, whole genome shotgun sequence.
DB (Fragment).
GN ORFNames=GSTENG00011027001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

RA Jallou O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Kellis M., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]

CC NUCLEOTIDE SEQUENCE.
CC Genoscope; Whitehead Institute Centre for Genome Research;
CC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAB01012653; CAP94726.1; -; Genomic_DNA.
DR NON TER 28
SQ SEQUENCE 28 AA; 3511 MW; 48861A48AD8FB624 CRC64;

Query Match 22.6%; Score 31; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 8.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIRALKWKN 9
Db 6 QURLLLWKN 14

RESULT 2

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Q9IN95_9HIV1
ID Q9IN95_9HIV1 PRELIMINARY; PRT; 28 AA.
AC Q9IN95;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
OS Name=gag;
GN Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99260287; PubMed=10331444; DOI=10.1089/08922299310953;
RA Mokili J.L., Wade C.M., Burns S.M., Cutting W.A., Bopopi J.M.,
RA Green S.D., Peutherer J.F., Simmonds P.;
RT "Genetic heterogeneity of HIV type 1 subtypes in Kimpese, rural
RT Democratic Republic of Congo."
RL AIDS Res. Hum. Retroviruses 15:655-664 (1999).
RN [2]
RA Mokili J.L.K.;
RP NUCLEOTIDE SEQUENCE.
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF144854; AAF69080.1; -; Genomic_DNA.
FT NON_TER 1
FT SEQUENCE 28 AA; 3322 MW; 76748DCB3296BAA9 CRC64;

Query Match 21.9%; Score 30; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 WKNAHL 12
Db 2 WKDSHL 7

RESULT 3
Q4XPP2_PLACH PRELIMINARY; PRT; 28 AA.
AC Q4XPP2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=PC107963.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5625;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karas M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86 (2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01004139; CAH81120.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 3428 MW; 5AF26F33A19D1787 CRC64;

Query Match 21.2%; Score 29; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 1.5e+04;
Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 LKWNALHKE 15
Db 1 LKWNALHKE 15

RESULT 4
Q4TT22_9SPHN PRELIMINARY; PRT; 28 AA.
AC Q4TT22;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=ELI0004;
OS Erythrobacter litoralis HTCC2594.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=314225;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HTCC2594;
RA Giovannoni S.J., Cho J.-C., Ferreira S., Johnson J., Kravitz S.,
RA Halpern A., Remington K., Beeson K., Trap B., Rogers Y.-H.,
RA Friedman R., Venter J.C.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAGG01000001; BAL76198.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 2729 MW; F7875483BF7ABE0E CRC64;

Query Match 21.2%; Score 29; DB 2; Length 28;
Best Local Similarity 38.5%; Pred. No. 1.5e+04;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 16 IAALEOEIAALEQ 28
Db 1 MAVAEEVVAEE 13

RESULT 5
Q4RCL2_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4RCL2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome undetermined SCAF18625, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00038553001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skallil Z., Cattolico L., Foulain J.P., De Berardinis V.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigou R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957 (2004).
RN [2]

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RP NUCLEOTIDE SEQUENCE
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01018625; CAG13871.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 28 AA; 3067 MW; 5BEFD973E2BD15CF CRC64;

Query Match 20.4%; Score 28; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 2.1e+04;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 6 KWKNAHLKQIEA 17
Db 9 RWGTCHPKPELS 20

RESULT 6
Q4YD65_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YD65;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB406027.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RA transcriptomic, and proteomic analyses.";
RA Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAI01006329; CAI04054.1; -; Genomic_DNA.
DR KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3374 MW; 3778B93D36F8559C CRC64;

Query Match 19.7%; Score 27; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 WKNLHL 12
Db 12 WENLHI 17

RESULT 7
Q4TIF5_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4TIF5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAf2190, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00038313001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

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OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RA the early vertebrate proto-karyotype.";
RA Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01002190; CAF87327.1; -; Genomic_DNA.
DR NON TER 28
FT NON TER 28
SQ SEQUENCE 28 AA; 3040 MW; 776D95631570A999 CRC64;

Query Match 19.7%; Score 27; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 2.8e+04;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 10 AHLKQIEAALQIEIA 24
Db 11 AEVRKLAELELELS 25

RESULT 8
Q8ZYI3_PYRAE PRELIMINARY; PRT; 28 AA.
AC Q8ZYI3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PAE0551.
GN OrderedLocustNames=PAE0551;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RA "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RA aerophilum.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009773; AAL62858.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 28 AA; 3001 MW; 869F81422C3A14D CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 29.4%; Pred. No. 3.7e+04;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 10 AHLKQIEAALQIEIAAL 26
Db 4 AEIKASVAELKAVGSL 20

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RESULT 9
Q7GHK5 AEDAL
ID Q7GHK5 AEDAL PRELIMINARY; PRT; 28 AA.
AC Q7GHK5
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Aedes albopictus (Forest day mosquito).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Culicinae; Culicini; Aedes; Stegomyia.
OX NCBI_TaxID=7160;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84307776; PubMed=6477610;
RA Heuchlen C.C.; Dublin D.T.;
RT "A cluster of four transfer RNA genes in mosquito mitochondrial DNA.";
RL Biochem. Int. 8:385-391(1984).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 3 family.
DR ENBL; M27317; AAA65504.2; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; Oxidored_q4; 1.
DR Hypothetical protein; Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
KW NON TER
FT NON TER
SQ SEQUENCE 28 AA; 3340 MW; BAFCF50953E376FF CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 3.7e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ALKWN 9
Db 23 ALEWNN 28

RESULT 10
Q42J3 PLABE
ID Q42J3 PLABE PRELIMINARY; PRT; 28 AA.
AC Q42J3
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB102380.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CRAI01000932; CAH95494.1; -; Genomic_DNA.
DR EMBL; CRAI01000932; CAH95494.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 28 AA; 3512 MW; 8CD8C5CFE90006F6 CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 41.7%; Pred. No. 3.7e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 ALKWNHLKOE 15
Db 8 ALNYNEARLKKD 19

RESULT 11
Q6AGW8 LEIXX
ID Q6AGW8 LEIXX PRELIMINARY; PRT; 28 AA.
AC Q6AGW8;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Lxx03670;
OS Leifsonia xyl (subsp. xyl).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furian L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carrier H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Lemos M.V.F., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
xyl subsp. xyl.";
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAT88377.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 28 AA; 3119 MW; 79BD5C47B0248C77 CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 38.5%; Pred. No. 3.7e+04;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 7 WKNHLKOEIAAL 19
Db 13 KYIHIKNAALFL 25

RESULT 12
Q9TWV5 PERAM
ID Q9TWV5 PERAM PRELIMINARY; PRT; 28 AA.
AC Q9TWV5;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE 10 kDa LEG regeneration protein (Fragment).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Blattinae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93075619; PubMed=1445782;
RA Nomura A., Kawasaki K., Kubo T., Natori S.;
RT "Purification and localization of p10, a novel protein that increases
in nymphal regenerating legs of Periplaneta americana (American
cockroach).";

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RL Int. J. Dev. Biol. 36:391-398(1992).
DR HSP; Q9NG96; INSV.
DR InterPro; IPR005055; A10_OS-D.
DR Pfam; PF03392; OS-D; 1.
SQ SEQUENCE 28 AA; 3367 MW; B0BEF9AD586758B7 CRC64;

Query Match 18.2%; Score 25; DB 2; Length 28;
Best Local Similarity 38.5%; Pred. No. 5e+04;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 KWKNAHLKQIEIA 18
Db 7 KYDNIKKEILAS 19

RESULT 13
Q4X6M9_PLACH PRELIMINARY; PRT; 28 AA.
AC Q4X6M9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC405735.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3469 MW; C55F38F38D3D91D5 CRC64;

Query Match 18.2%; Score 25; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 5e+04;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWKNNAHLKQIEI 16
Db 5 KRKYKKKLYKWDI 20

RESULT 14
Q4XCC8_PLACH PRELIMINARY; PRT; 28 AA.
AC Q4XCC8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC403471.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA Jansse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3469 MW; C55F38F38D3D91D5 CRC64;

Query Match 18.2%; Score 25; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 5e+04;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWKNNAHLKQIEI 16
Db 5 KRKYKKKLYKWDI 20

RESULT 15
Q6U7R1_CRYNV PRELIMINARY; PRT; 48 AA.
AC Q6U7R1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-24 sterol reductase (Fragment).
GN Name=ERG4;
OS Cryptococcus neoformans var. grubii H99.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=235443;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H99;
RA Stuart L.T., Allen A., Dietrich F.S.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY376721; AAQ88132.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR01171; ERG4_ERG24.
DR Pfam; PF01222; ERG4_ERG24; 1.
FT NON TER 1
SQ SEQUENCE 28 AA; 3430 MW; E645861ED8FF19DC CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.7e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RALKWK 8
Db 17 KVKWK 22

RESULT 16
Q00440_GLOLA PRELIMINARY; PRT; 48 AA.
AC Q00440;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAS protein (Fragment).
GN Name=C1ras1;
OS Glomerella lagenarium (Anthracnose fungus) (Colletotrichum
OS lagenarium).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
OX NCBI_TaxID=5462;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Mycelium;
RA Lee C.-W., Kim J.-S., Jung B.-K., Park S.-H.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U33745; AAA74985.1; -; Genomic_DNA.
DR HSSP: P01112; 1PLK.
DR GO: GO:0005525; F:GTP binding; IEA.
DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro: IPR001806; Ras_trnsfrmg.
DR Pfam: PF00071; Ras; 1.
KW GTP-binding; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3199 MW; 77197F0558CAAADC CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 6.7e+04;
Matches 5; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

QY 9 NAHLKQEIQAALQEIQAAL 27
DQ 1 DSYRKQ--CVIDEVALD 17

RESULT 17
Q9TWE2_PARLI PRELIMINARY; PRT; 28 AA.
AC Q9TWE2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE AXONEMAL alpha-tubulin isoform (fragment).
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96215272; PubMed=8626629; DOI=10.1074/jbc.271.17.9928;
RA Mary J., Redeker V., Le Caer J.P., Rossier J., Schmitter J.M.;
RT "Posttranslational modifications in the C-terminal tail of axonemal
RT tubulin from sea urchin sperm".
RL J. Biol. Chem. 271:9928-9933(1996).
DR GO: GO:0005874; C:microtubule; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0007018; P:microtubule-based movement; IEA.
DR InterPro: IPR002452; Alpha tubulin.
DR PANTHER: PTHR11588.SF1; Alpha tubulin.
SQ SEQUENCE 28 AA; 3104 MW; 5C50E220D1AFD7C1 CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.7e+04;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIAALRQE 22
DQ 1 DLAALEKD 8

RESULT 18
Q99LW3_MOUSE PRELIMINARY; PRT; 28 AA.
AC Q99LW3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002195; AAH02195.1; -; mRNA.
DR Ensembl: ENSMUSG00000057032; Mus musculus.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 3503 MW; 737D5EC9A6ECFD9B CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 23.1%; Pred. No. 6.7e+04;
Matches 3; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRALKWKNAHLKQ 14
DQ 12 VTTLRWRAQNYEQ 24

RESULT 19
Q4T3N5_TETNG
ID Q4T3N5_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4T3N5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF9978, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00007715001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fieher S., Lutfalla G., Dossat C., Segrens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Foulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudat V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

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RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RL the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01009978; CAP92497.1; -; Genomic_DNA.
 FT NON_TER 1 28
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3037 MW; 996533BD98146314 CRC64;
 Query Match 17.5%; Score 24; DB 2; Length 28;
 Best Local Similarity 31.2%; Pred. No. 6.7e+04;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 12 LKQEIATLEOEIAALE 27
 Db ::::: :
 3 LREAVALLTAQOTSLE 18
 RESULT 20
 Q53TM9 HUMAN PRELIMINARY; PRT; 28 AA.
 AC Q53TM9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein FLJ13984 (Fragment).
 GN Name=FLJ13984;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Walker C., Drone K., Page K.;
 RA "The sequence of Homo sapiens BAC clone RP11-284E18.";
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.;
 RA Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC008065; AAX93077.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3288 MW; BDBE4ACFFC20A84D CRC64;
 Query Match 16.8%; Score 23; DB 2; Length 28;
 Best Local Similarity 26.3%; Pred. No. 8.9e+04;
 Matches 5; Conservative 6; Mismatches 4; Indels 4; Gaps 1;
 QY 5 LKWKNAHLKQEIATLEOEI 23
 Db ::::: :
 1 MQWS-----KEEEAARKKV 15
 RESULT 21
 Q4XCS0 PLACH PRELIMINARY; PRT; 28 AA.
 ID Q4XCS0 PLACH PRELIMINARY; PRT; 28 AA.

AC Q4XCS0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC403293.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemodsporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAJ01007505; CAH85302.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 28 AA; 2982 MW; 1ED93C8890D0D509 CRC64;
 Query Match 16.8%; Score 23; DB 2; Length 28;
 Best Local Similarity 41.2%; Pred. No. 8.9e+04;
 Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 11 HLKQEIATLEOEIAALE 27
 Db ::::: :
 9 NLVEESLALLKEIYLCE 25
 RESULT 22
 Q4YAC7 PLABE PRELIMINARY; PRT; 28 AA.
 ID Q4YAC7 PLABE PRELIMINARY; PRT; 28 AA.
 AC Q4YAC7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB401815.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemodsporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAI01007122; CAI05297.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 28 AA; 3288 MW; 52CB801BB1CD1F21 CRC64;
 Query Match 16.8%; Score 23; DB 2; Length 28;
 Best Local Similarity 41.7%; Pred. No. 8.9e+04;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KIRALKWKNAHL 12

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Db      || : || | :
13 KITLIKGRARI 24

RESULT 23
Q941S1_PINRA
ID Q941S1_PINRA PRELIMINARY; PRT; 28 AA.
AC Q941S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nonspecific lipid transfer protein (Fragment).
OS Pinus radiata (Monterey pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=3347;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jones D.F.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029020; AAK40292.1; -; Genomic_DNA.
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2989 MW; 89853214D0F65986 CRC64;

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 8.9e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 WKNAHL 12
DB 3 WKAANL 8

RESULT 24
Q4NC96_9MICC
ID Q4NC96_9MICC PRELIMINARY; PRT; 28 AA.
AC Q4NC96;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=ArthDRAFT_0836;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA US DOE Joint Genome Institute (PGF-ORNL);
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pfluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA US DOE Joint Genome Institute (PGF-ORNL);
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHG01000016; EAL95000.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 2977 MW; 89C905D398BE0BA4 CRC64;

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 18 ALEQETIAALE 27
DB 18 ATEETSLSLE 27

RESULT 26
Q91VP0_MOUSE
ID Q91VP0_MOUSE PRELIMINARY; PRT; 28 AA.
AC Q91VP0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=Mobk1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diachenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Kzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RA Director MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011285; AAH11285.1; -; mRNA.
DR MGI; MGI:2442631; Mobjk1b.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 2809 MW; 97A97BBE33A3P19F CRC64;

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 8.9e+04;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 16 IAALQEIAALE 27
Db 9 LAAPRQYGALD 20

RESULT 27
Q7S105_NEUCR
ID Q7S105_NEUCR PRELIMINARY; PRT; 28 AA.
AC Q7S105;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU00647.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zeiter A., Schulte U.,
RA Kothé G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Navig D.O., Alex L.A., Mannheimaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC CC
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000001; EAA36551.1; -; Genomic DNA.
SQ SEQUENCE 28 AA; 3235 MW; C3CD3869AFC94760 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 11 HLKQEI1A 18

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Db 5 HLKHAURA 12

RESULT 28
P87021_MAGGR
ID P87021_MAGGR PRELIMINARY; PRT; 28 AA.
AC P87021;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAS protein (Fragment).
GN Name=MGRAS1;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariaceae; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-6; TISSUE=Mycelium;
RX MEDLINE=97306448; PubMed=9163749;
RA Park S.Y., Lee E.J., Lee C.W.;
RT "Molecular cloning and sequence analysis of a putative ras gene of the
RT phytopathogenic fungus Botryotinia fuckeliana."
RL Mol. Cells 7:300-304(1997).
DR EMBL; U79559; AAB51237.1; -; Genomic_DNA.
DR HSSP; P01112; 1PLK.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001806; Ras_trnsmrg.
DR Pfam; PF00071; Ras; 1.
KW GTP-binding; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3175 MW; 7718A47558CAADC CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 1.2e+05;
Matches 5; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

Qy 9 NAHLKQEI1AALQEI1A 27
Db 1 DSYRKQ-CVIDDEVALLD 17

RESULT 29
Q4Y377_PLACH
ID Q4Y377_PLACH PRELIMINARY; PRT; 28 AA.
AC Q4Y377;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PCI02434.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC CC
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01001405; CAH76383.1; -; Genomic_DNA.
KW Hypothetical protein.

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FT NON TER 1
SQ SEQUENCE 28 AA; 3439 MW; 8F5EBB72572F8B4C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 KNAHL 12
Db :|||:
9 RNAHI 13

RESULT 30
Q4YE24_PLABE
ID Q4YE24_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YE24;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB404883.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI03425.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3491 MW; A2D2C1861CEDF94C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 WKNAH 11
Db :|||:
15 WKSAN 19

RESULT 31
Q4YQS2_PLABE
ID Q4YQS2_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YQS2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB107544.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
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RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01002911; CAH99635.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 28
SQ SEQUENCE 28 AA; 3252 MW; 40E0D8480B5DFA21 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 WKNAH 11
Db :|||:
17 YKNSH 21

RESULT 32
Q4Z0C3_PLABE
ID Q4Z0C3_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4Z0C3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB103349.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01001345; CAH96267.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3430 MW; 2C2E6C5C95CCB88E CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 KWNAHL 12
Db :|||:
12 KKNHI 18

RESULT 33
O62731_CANFA
ID O62731_CANFA PRELIMINARY; PRT; 28 AA.
AC O62731;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tropomyosin (fragment).
GN Name=TPM1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
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RN NUCLEOTIDE SEQUENCE.
RP Liu P.-C., Chen Y.-W., Grob S.E., Katz M.L., Johnson G.S.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF049587; AAC05499.1; -; Genomic DNA.
DR Ensembl; ENSCAPG0000016966; Canis familiaris.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin, 1.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3251 MW; 5694A77F1CA73D30 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 1.2e+05;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 13 LKQEIATLEQEI 23
Db 12 ESKCAELEEL 22

RESULT 34
Q9GMF5 PAPH PRELIMINARY; PRT; 28 AA.
AC Q9GMF5
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Rh50 glycoprotein (Fragment).
GN Name=RHAG;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363873; PubMed=10903374;
RA Huang C.H., Liu Z., Apoll P.A., Blancher A.;
RT "Sequence, organization, and evolution of Rh50 glycoprotein genes in
nonhuman primates.";
RL J. Mol. Evol. 51:76-87(2000).
DR EMBL; AF177632; AAG00314.1; -; Genomic DNA.
FT NON_TER 28
FT NON_TER 28
SQ SEQUENCE 28 AA; 3332 MW; EB74D4E45F83A90C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LKQEIATLEQEI 26
Db 3 LKFLPMAIVLEIAM 17

RESULT 35
Q9GMF6 MACMU PRELIMINARY; PRT; 28 AA.
AC Q9GMF6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Rh50 glycoprotein (Fragment).
GN Name=RHAG;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363873; PubMed=10903374;
RA Huang C.H., Liu Z., Apoll P.A., Blancher A.;

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RT "Sequence, organization, and evolution of Rh50 glycoprotein genes in
nonhuman primates.";
RL J. Mol. Evol. 51:76-87(2000).
DR EMBL; AF177631; AAG00313.1; -; Genomic DNA.
FT NON_TER 28
FT NON_TER 28
SQ SEQUENCE 28 AA; 3332 MW; EB74D4E45F83A90C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LKQEIATLEQEI 26
Db 3 LKFLPMAIVLEIAM 17

RESULT 36
Q9XGE6 VICFA PRELIMINARY; PRT; 28 AA.
AC Q9XGE6
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Ribonuclease H (fragment).
GN Name=RNase H;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pearce S.R., Stuart-Rogers C., Knox M., Kumar A., Ellis T.H.,
RA Flavell A.J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243100; CAB45144.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 28 AA; 3265 MW; AA26A6A8F2F280D6 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 12 LKQEIATLEQEI 23
Db 16 IRRELGLDNKI 27

RESULT 37
Q50102 MYCLE PRELIMINARY; PRT; 48 AA.
AC Q50102
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE U650k.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15184; AAA63067.1; -; Genomic DNA.
SQ SEQUENCE 28 AA; 3515 MW; F732EAA14A754562 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 21.4%; Pred. No. 1.2e+05;

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Matches 3; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 2 IRALKWNAHLKOE 15
Db 12 LRHLRQHRRHVRD 25

RESULT 38
Q93JY6 MYCTU
ID Q93JY6_MYCTU PRELIMINARY; PRT; 28 AA.
AC Q93JY6;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE DNA-directed RNA polymerase (Fragment).
GN Names=rpob;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21367865; PubMed=11474030;
RX DOI=10.1128/JCM.39.8.2987-2990.2001;
RA Mani C., Selvakumar N., Narayanan S., Narayanan P.R.;
RT "Mutations in the rpoB gene of multidrug-resistant Mycobacterium
tuberculosis clinical isolates from India.";
RL J. Clin. Microbiol. 39:2987-2990(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chervu M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ297928; CAC50349.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006350; F:transcription; IEA.
DR InterPro; IPR007645; RNA_pol_Rpb2_3.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
KW DNA-directed RNA polymerase.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3129 MW; 64E6333409DFD446 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 13 KQBIAMLE 20
Db 21 KRLSLALE 28

RESULT 39
Q724AL LISMF
ID Q724AL_LISMF PRELIMINARY; PRT; 28 AA.
AC Q724AL;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LMOF2365_0323;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
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Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Iran B., Kathariou S., Wonderling L.D., Unlich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL; AB017323; AAT03110.1; -; Genomic_DNA.
DR TIGR; LMOF2365_0323; -.
KW Complete proteome.
SQ SEQUENCE 28 AA; 3243 MW; E699E78C805C13B9 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 12 LKQETAAALRQEI 23
Db 1 MKLLFATLVEI 12

RESULT 40
Q4RFB7 TETNG
ID Q4RFB7_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4RFB7;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome 8 SCAP15119, whole genome shotgun sequence.
GN ORFNames=GSTENG00035394001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE0105119; CAG12915.1; -; Genomic_DNA.
SQ SEQUENCE 28 AA; 2884 MW; 3755860F01ADC3D CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 IRALKW 7
Db 10 ITALSW 15

RESULT 41
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Q4SVA3_TETNG
ID Q4SVA3_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4SVA3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF13770, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG00012080001;
GN Tetraodon nigroviridis (Green puffer).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01013770; CAF95429.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3250 MW; C50C59229401CF6D CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ALKWKNAH 11
| : |
| : |
Db 4 AKWESEPH 11

RESULT 42
QSF210_MOUSE
ID QSF210_MOUSE PRELIMINARY; PRT; 28 AA.
AC QSF210;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Oxytocin binding protein 2 (Fragment).
GN Name=Osbp2; ORFNames=RP23-309E11.7-004;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dunn M.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731853; CAI51856.1; -; Genomic_DNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 3453 MW; 2BF5DACD2D68FCFC CRC64;

Query Match 15.7%; Score 21.5; DB 2; Length 28;
Best Local Similarity 45.5%; Pred. No. 1.4e+05;
Matches 5; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 6 KWKNA-HLKOE 15
| : |
| : |
Db 18 KWQRALNYEQE 28

RESULT 43
GRP_ALIMI
ID GRP_ALIMI STANDARD; PRT; 28 AA.
AC P31886;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gastrin-releasing peptide (GRP) [Contains: Neuromedin C (GRP-10)].
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylia; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369; DOI=10.1016/0196-9781(93)90147-9;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
RL and stomach of the alligator.";
RL Peptides 14:573-579(1993).
CC -! FUNCTION: GRP stimulates gastrin release as well as other
CC gastrointestinal hormones.
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC InterPro: IPR000874; Bombesin.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amidation; Bombesin family; Direct protein sequencing.
FT PEPTIDE 19 28 Neuromedin C.
FT MOD RES 28 28 Methionine amide.
SQ SEQUENCE 28 AA; 2786 MW; A74DB0487D84963 CRC64;

Query Match 15.3%; Score 21; DB 1; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 RALKWKNAHL 12
| : |
| : |
Db 18 RGSWAVGHL 27

RESULT 44
Q5AW44_EMENI
ID Q5AW44_EMENI PRELIMINARY; PRT; 28 AA.
AC Q5AW44;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Predicted protein.
GN ORFNames=AN7486.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearrellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACD01000129; EAA62066.1; -; Genomic DNA.
SQ SEQUENCE 28 AA; 3333 MW; 47DC557430549950 CRC64;

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 8 KNAHLKQE 15
Db 16 RDGHIRQ 23

RESULT 45
Q9TWX0 MANSE
ID Q9TWX0_MANSE PRELIMINARY; PRT; 28 AA.
AC Q9TWX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cell surface protein 2F5 91 kDa component (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingoidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92331807; PubMed=1628754;
RA Nardi J.B.;
RT "Dynamic expression of a cell surface protein during rearrangement of
RT epithelial cells in the Manduca wing monolayer.";
RL Dev. Biol. 152:161-171(1992).
DR PIR; A44877; A44877.
FT NON_TER 1
FT TER 28
SQ SEQUENCE 28 AA; 3271 MW; 28D250E730959651 CRC64;

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 27.8%; Pred. No. 1.6e+05;
Matches 5; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 7 WKNA---HLKQEIAALE 20
Db 5 WRVADESLEVEQIESFE 22

Search completed: November 21, 2005, 21:46:24
Job time : 144 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:25:48 ; Search time 31.5 Seconds
(without alignments)
73.489 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWNAHLKQETIAALQETIALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 4644

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pdp.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	32.8	28	2	US-08-486-099-84
2	45	32.8	28	2	US-08-360-107A-94
3	45	32.8	28	2	US-08-484-223B-84
4	45	32.8	28	2	US-08-919-597-84
5	45	32.8	28	2	US-08-475-668A-84
6	45	32.8	28	2	US-08-485-551A-84
7	45	32.8	28	2	US-08-471-913A-84
8	45	32.8	28	2	US-08-485-264A-84
9	45	32.8	28	2	US-08-474-349A-84
10	45	32.8	28	2	US-08-255-208A-20
11	45	32.8	28	2	US-08-470-896-84
12	45	32.8	28	2	US-09-914-259-1
13	45	32.8	28	2	US-08-485-546A-84
14	45	32.8	28	2	US-09-350-841A-1549
15	45	32.8	28	2	US-09-350-841A-1566
16	45	32.8	28	2	US-09-350-841A-1573
17	45	32.8	28	2	US-08-487-266A-84
18	45	32.8	28	2	US-08-484-741-84
19	44	32.1	28	1	US-08-182-175A-1
20	44	32.1	28	4	PCT-US92-06412-1
21	38	27.7	28	1	US-08-182-175A-3
22	38	27.7	28	1	US-08-474-633A-70
23	38	27.7	28	2	US-08-823-771-70
24	38	27.7	28	4	PCT-US92-06412-3
25	37	27.0	28	1	US-07-977-630-53
26	36	26.3	28	1	US-08-182-175A-2
27	36	26.3	28	1	US-08-182-175A-39

28	36	26.3	28	1	US-08-182-175A-43	Sequence 43, Appl
29	36	26.3	28	1	US-08-182-175A-47	Sequence 47, Appl
30	36	26.3	28	1	US-08-474-633A-36	Sequence 36, Appl
31	36	26.3	28	1	US-08-474-633A-40	Sequence 40, Appl
32	36	26.3	28	1	US-08-474-633A-56	Sequence 56, Appl
33	36	26.3	28	1	US-08-474-633A-67	Sequence 67, Appl
34	36	26.3	28	1	US-08-944-133-18	Sequence 18, Appl
35	36	26.3	28	2	US-08-823-771-36	Sequence 36, Appl
36	36	26.3	28	2	US-08-823-771-40	Sequence 40, Appl
37	36	26.3	28	2	US-08-823-771-56	Sequence 56, Appl
38	36	26.3	28	2	US-08-823-771-67	Sequence 67, Appl
39	36	26.3	28	4	PCT-US92-06412-2	Sequence 2, Appl
40	36	26.3	28	4	PCT-US92-06412-39	Sequence 39, Appl
41	36	26.3	28	4	PCT-US92-06412-43	Sequence 43, Appl
42	36	26.3	28	4	PCT-US92-06412-47	Sequence 47, Appl
43	35	25.5	28	1	US-08-944-133-31	Sequence 31, Appl
44	35	25.5	28	1	US-08-944-133-35	Sequence 35, Appl
45	35	25.5	28	2	US-09-082-279B-377	Sequence 377, App

ALIGNMENTS

RESULT 1
US-08-486-099-84
; Sequence 84, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULAR TYPE: peptide
US-08-486-099-84

Query Match 32.8% ; Score 45; DB 2; Length 28;

Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 21
|:| || ||:|:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 2

US-08-360-107A-94
; Sequence 94, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-360-107A-94

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 21
|:| || ||:|:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 3

US-08-484-223B-84
; Sequence 84, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-484-223B-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 21
|:| || ||:|:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 4

US-08-919-597-84
; Sequence 84, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: peptide
; US-08-919-597-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 1 KIRALKWKNHKLKOEIAALEQ 21
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 5
US-08-475-668A-84
; Sequence 84, Application US/08475668A
; Patent No. 606065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

US-08-475-668A-84
; Sequence 84, Application US/08475668A
; Patent No. 606065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

US-08-475-668A-84
; Sequence 84, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-551A-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 1 KIRALKWKNHKLKOEIAALEQ 21
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 6
US-08-485-551A-84
; Sequence 84, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-551A-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 1 KIRALKWKNHKLKOEIAALEQ 21
Db 7 KVEELLSKNYHLENEVARLKK 27
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RESULT 12
US-09-914-259-1
; Sequence 1, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-914-259-1

Query Match      32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 KIRALKWKNAHLKQETAALEQ 21
       |:| ||| |:| |:| |:|
Db      7 KVEELLSKNYHLENEVARLKK 27

RESULT 13
US-08-485-546A-84
; Sequence 84, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING RPSSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid

RESULT 14
US-09-350-841A-1549
; Sequence 1549, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1549
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1549

Query Match      32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 KIRALKWKNAHLKQETAALEQ 21
       |:| ||| |:| |:| |:|
Db      7 KVEELLSKNYHLENEVARLKK 27

RESULT 15
US-09-350-841A-1566
; Sequence 1566, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1566
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1566

Query Match      32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 KIRALKWKNAHLKQETAALEQ 21
       |:| ||| |:| |:| |:|
Db      7 KVEELLSKNYHLENEVARLKK 27

RESULT 16
US-09-350-841A-1573
; Sequence 1573, Application US/09350841A
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US-08-487-266A-84

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; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 4)4"
;
; US-08-182-175A-1
;
; Query Match 32.1%; Score 44; DB 1; Length 28;
; Best Local Similarity 36.0%; Pred. No. 22;
; Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
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; QY 1 KIRALKKWAHLKQETAALEQETAA 25
; Db 4 KKLAKLEKLEKLEKLEKLEKLEKLA 28
;
; RESULT 20
; PCT-US92-06412-1
; Sequence 1, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
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; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 4)4"
;
; PCT-US92-06412-1
;
; Query Match 32.1%; Score 44; DB 4; Length 28;
; Best Local Similarity 36.0%; Pred. No. 22;
; Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
;
; QY 1 KIRALKKWAHLKQETAALEQETAA 25
; Db 4 KKLAKLEKLEKLEKLEKLEKLEKLA 28
;
; RESULT 21
; US-08-182-175A-3
; Sequence 3, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
```

Query Match 27.7%; Score 38; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETIALEQETAA 25
|::||:|::|::|::|::|::|
Db 4 KLKAMEBKLMAMEBKLMAMEBKLA 28

RESULT 24

PCT-US92-06412-3
; Sequence 3, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7) 4"
PCT-US92-06412-3

Query Match 27.7%; Score 38; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETIALEQETAA 25
|::||:|::|::|::|::|::|
Db 4 KLKAMEBKLMAMEBKLMAMEBKLA 28

RESULT 25

US-07-977-630-53
; Sequence 53, Application US/07977630
; Patent No. 5583038
; GENERAL INFORMATION:
; APPLICANT: Stover, Charles K.
; TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING

; TITLE OF INVENTION: DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,630
; FILING DATE: No. 5583038ember 17, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Herron, Charles J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 469201-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-977-630-53

Query Match 27.0%; Score 37; DB 1; Length 28;
Best Local Similarity 56.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 11 HLKQETIALEQETIAAL 26
|||::|::|::|::|::|
Db 5 HLAETATMQEITL 20

RESULT 26

US-08-182-175A-2
; Sequence 2, Application US/08182175A
; Patent No. 5559223

; GENERAL INFORMATION:

; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler

; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E.I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: Macintosh System, 6.0

; SOFTWARE: Microsoft Word, 4.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/182,175A

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/743,006

; FILING DATE: 9 August 1991

; ATTORNEY/AGENT INFORMATION:

; 10000. 057420
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-182-175A-43

APPLICANT: Janet A. Rice

```
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing H
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-182-175A-47

Query Match      26.3%; Score 36; DB 1; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY      1 KIRALKWNAHLKQEIATLALEQETAA 25
        |::||:| |::||:| |::||:|
Db      4 KXKAMEEKXKAMEEKXKAMEEKXKA 28

RESULT 30
US-08-474-633A-36
; Sequence 36, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; TITLE OF INVENTION: CHIMERIC GENES AND
; TITLE OF INVENTION: METHODS FOR INCREASING
; TITLE OF INVENTION: INCREASING THE LYSINE
; TITLE OF INVENTION: AND THREONINE CONTENT
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-633A-40
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; APPLICATION NUMBER: US/08/474,633A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-633A-36

Query Match      26.3%; Score 36; DB 1; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY      1 KIRALKWNAHLKQEIATLALEQETAA 25
        |::||:| |::||:| |::||:|
Db      4 KXKAMEEKXKAMEEKXKAMEEKXKA 28

RESULT 31
US-08-474-633A-40
; Sequence 40, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; TITLE OF INVENTION: CHIMERIC GENES AND
; TITLE OF INVENTION: METHODS FOR INCREASING
; TITLE OF INVENTION: INCREASING THE LYSINE
; TITLE OF INVENTION: AND THREONINE CONTENT
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-633A-40
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RESULT 35
US-08-823-771-36
; Sequence 36, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; METHODS FOR INCREASING
; INCREASING THE LYSINE
; AND THEONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C

Query Match	26.3%	Score 36;	DB 2;	Length 28;
Best Local Similarity	24.0%	Pred. No. 2.6e+02;		


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; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 5)4"
PCT-US92-06412-2

Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNVHLKQETAALEQETAA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKKA 28

RESULT 40
PCT-US92-06412-39
; Sequence 39, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-43

Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNVHLKQETAALEQETAA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKKA 28

RESULT 41
PCT-US92-06412-43
; Sequence 43, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-43

Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNVHLKQETAALEQETAA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKKA 28
```

```
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-39

Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNVHLKQETAALEQETAA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKKA 28

RESULT 41
PCT-US92-06412-43
; Sequence 43, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-43

Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNVHLKQETAALEQETAA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKKA 28
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 387-3221
TELEFAX: 504 346-8049
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-944-133-31

Query Match 25.5%; Score 35; DB 1; Length 28;
Best Local Similarity 34.6%; Pred. No. 3.Se+02;
Matches 9; Conservative 8; Mismatches 9; Indels

QY 3 RALKWKNNAHLKQEIQAALQEQIAALEQ 28
DB 1 KALKKALKKALKKALKKALKK 26

RESULT 44
US-08-944-133-35
Sequence 35, Application US/089441133
Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
APPLICANT: Becker, Calvin L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
STATE: LA
COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H

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Search completed: November 21, 2005, 21:41:32
Job time : 32.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:41:39 ; Search time 106.5 Seconds
(without alignments)
109.852 Million cell updates/sec

Title: US-10-088-417A-4

Perfect score: 137

Sequence: 1 KIRALKWNAHLKQETAALEQ 28

Scoring table: BLOSUM62

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 5696

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	59.1	28	4	US-10-360-053-23
2	59	43.1	28	4	US-10-360-053-21
3	54	39.4	28	4	US-10-360-053-22
4	45	32.8	28	4	US-10-080-608A-1
5	45	32.8	28	4	US-10-370-685-90
6	45	32.8	28	4	US-10-267-682-84
7	45	32.8	28	4	US-10-267-748-84
8	39	28.5	28	3	US-09-320-907B-6
9	39	28.5	28	4	US-10-447-292-6
10	38	27.7	28	4	US-10-023-066A-70
11	38	27.7	28	5	US-10-804-678-70
12	36	26.3	28	4	US-10-023-066A-36
13	36	26.3	28	4	US-10-023-066A-40
14	36	26.3	28	4	US-10-023-066A-56
15	36	26.3	28	4	US-10-023-066A-67
16	36	26.3	28	5	US-10-804-678-36
17	36	26.3	28	5	US-10-804-678-40
18	36	26.3	28	5	US-10-804-678-56
19	36	26.3	28	5	US-10-804-678-67
20	35	25.5	28	4	US-10-351-641-377
21	34	24.8	28	3	US-09-847-940B-19
22	34	24.8	28	3	US-09-945-917-24
23	34	24.8	28	3	US-09-847-946A-19
24	34	24.8	28	4	US-10-652-244-16
25	34	24.8	28	5	US-10-830-959-6
26	34	24.8	28	5	US-10-979-683-19
27	34	24.8	28	5	US-10-900-399-16

28	34	24.8	28	6	US-11-032-630-32	Sequence 32, Appl
29	33.5	24.5	28	3	US-09-864-761-42292	Sequence 42292, A
30	33	24.1	28	4	US-10-267-682-85	Sequence 85, Appl
31	33	24.1	28	4	US-10-267-748-85	Sequence 85, Appl
32	32	23.4	28	4	US-10-023-066A-58	Sequence 58, Appl
33	32	23.4	28	4	US-10-552-244-17	Sequence 17, Appl
34	32	23.4	28	5	US-10-804-678-58	Sequence 58, Appl
35	32	23.4	28	5	US-10-900-399-17	Sequence 17, Appl
36	31	22.6	28	3	US-09-864-761-43156	Sequence 43156, A
37	31	22.6	28	4	US-10-252-136-16	Sequence 16, Appl
38	31	22.6	28	4	US-10-351-641-494	Sequence 494, App
39	31	22.6	28	4	US-10-267-682-163	Sequence 163, App
40	31	22.6	28	4	US-10-267-748-163	Sequence 163, App
41	30	21.9	28	3	US-09-746-742-25	Sequence 25, Appl
42	30	21.9	28	4	US-10-080-608A-2	Sequence 2, Appl
43	30	21.9	28	4	US-10-370-685-91	Sequence 91, Appl
44	30	21.9	28	4	US-10-267-682-86	Sequence 86, Appl
45	30	21.9	28	4	US-10-267-748-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1

US-10-360-053-23

Sequence 23, Application US/10360053

Publication No. US20030170230A1

GENERAL INFORMATION:

APPLICANT: Caterer, Nigel

APPLICANT: Uttenhal, Lars O

APPLICANT: Nielsen, Rasmus W

TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antib

TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi

TITLE OF INVENTION: Thereof

FILE REFERENCE: IMX-0028

CURRENT APPLICATION NUMBER: US/10/360,053

CURRENT FILING DATE: 2003-02-05

PRIOR APPLICATION NUMBER: US60/354,376

PRIOR FILING DATE: 2002-02-05

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.1

SEQ ID NO 23

LENGTH: 28

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-360-053-23

Query Match 59.1%; Score 81; DB 4; Length 28;

Best Local Similarity 64.0%; Pred. No. 0.0011;

Matches 16; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ALRWNAHLKQETAALEQ 28

1 A1KYQAARKNEIAAKQETAAIEQ 25

RESULT 2

US-10-360-053-21

Sequence 21, Application US/10360053

Publication No. US20030170230A1

GENERAL INFORMATION:

APPLICANT: Caterer, Nigel

APPLICANT: Uttenhal, Lars O

APPLICANT: Nielsen, Rasmus W

TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antib

TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi

TITLE OF INVENTION: Thereof

FILE REFERENCE: IMX-0028

CURRENT APPLICATION NUMBER: US/10/360,053

CURRENT FILING DATE: 2003-02-05

PRIOR APPLICATION NUMBER: US60/354,376

TELEFAX: (212) 869-9741/8964
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 84:

US-10-267-748-84

Query Match 32.8%; Score 45; DB 4; Length 28;
Best Local Similarity 42.9%; Pred.No. 65;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQEIAALEEQ 21
| : | || || : | : | :
Db 7 KVEELLKKNYHLENEVARLKK 27

RESULT 8

US-09-320-907B-6
Sequence 6, Application US/09320907B
Publication No. US20020198360A1
GENERAL INFORMATION:
APPLICANT: GINSBERG, MARK H.
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF TRANSMEMBRANE RECEPTORS
FILE REFERENCE: SRI-0006
CURRENT APPLICATION NUMBER: US/09/320,907B
CURRENT FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 09/187,236
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-320-907B-6

Query Match 28.5%; Score 39; DB 3; Length 28;
Best Local Similarity 37.0%; Pred.No. 4e+02;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0

QY 1 KIRALKKNAHLKQEIAALEQEAAL 27
| : | : | : | : | : | :
Db 1 KLEALEGRDLLEGKLEALEGKD 27

RESULT 9

US-10-447-292-6
Sequence 6, Application US/10447292
Publication No. US20030224453A1
GENERAL INFORMATION:
APPLICANT: GINSBERG, MARK H.
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF TRANSMEMBRANE RECEPTORS
FILE REFERENCE: SRI-0006
CURRENT APPLICATION NUMBER: US/10/447,292
CURRENT FILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: US/09/320,907B
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 09/187,236
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6

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/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-447-292-6

Query Match      28.5%; Score 39; DB 4; Length 28;
Best Local Similarity 37.0%; Pred. No. 4e+02;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETAALEQETAALE 27
Db 1 KLEALEGRDLAEGKLEALBKGLDALE 27

RESULT 10
US-10-023-066A-70
; Sequence 70, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSEINE CONTENT OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-023-066A-70

Query Match      27.7%; Score 38; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETAALEQETAA 25
Db 1 KLEALEGRDLAEGKLEALBKGLDALE 27

RESULT 11
US-10-804-678-70
; Sequence 70, Application US/10804678
; Publication No. US2005005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSEINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-804-678-70

Query Match      27.7%; Score 38; DB 5; Length 28;
Best Local Similarity 24.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETAALEQETAA 25
Db 4 KLEALEGRDLAEGKLEALBKGLDALE 28

RESULT 12
US-10-023-066A-36
; Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
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Db 4 KLEALEGRDLAEGKLEALBKGLDALE 28

RESULT 11
US-10-804-678-70
; Sequence 70, Application US/10804678
; Publication No. US2005005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSEINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-804-678-70

Query Match      27.7%; Score 38; DB 5; Length 28;
Best Local Similarity 24.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETAALEQETAA 25
Db 4 KLEALEGRDLAEGKLEALBKGLDALE 28

RESULT 12
US-10-023-066A-36
; Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
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2


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;
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 5)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-804-678-67

Query Match 26.3%; Score 36; DB 5; Length 28;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQEIATALEQETAA 25
Db 4 KWKAMEEKWKAMEEKWKAMEEKMA 28

RESULT 20
US-10-351-641-377
; Sequence 377, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 377
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-377

Query Match 25.5%; Score 35; DB 4; Length 28;
Best Local Similarity 43.8%; Pred. No. 1.4e+03;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQEI 16
Db 1 KVEELLSKNYHLENEL 16

RESULT 21
US-09-847-940B-19
; Sequence 19, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
```

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;
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptides
US-09-847-940B-19

Query Match 24.8%; Score 34; DB 3; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 3 RALKWNAHLKQEIATALEQ 22
Db 11 RRMKWKKTA--DASALQTE 28

RESULT 22
US-09-945-917-24
; Sequence 24, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-945-917-24

Query Match 24.8%; Score 34; DB 3; Length 28;
Best Local Similarity 38.9%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 IRALKWNAHLKQETAAAL 19
Db 5 VNKIKTENKQLKKEVDKL 22

RESULT 23
US-09-847-946A-19
; Sequence 19, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19

Query Match      24.8%; Score 34; DB 3; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

Qy      3 RALKWKNHLKQEIATALEQE 22
Db      11 RRMWKKTL--DASALQTE 28

RESULT 24
US-10-652-244-16
; Sequence 16, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-652-244-16

Query Match      24.8%; Score 34; DB 4; Length 28;
Best Local Similarity 39.1%; Pred. No. 1.9e+03;
Matches 9; Conservative 6; Mismatches 4; Indels 4; Gaps 1;

Qy      10 AHLKQEIATALEQEI----AALEQ 28
Db      3 ASLRQQLALQGLQHLQALISQ 25

RESULT 25
US-10-830-959-6
; Sequence 6, Application US/10830959
; Publication No. US20040259201A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Howard
; APPLICANT: Nadesalingam, Palaniyar
; APPLICANT: Reid, Kenneth
; APPLICANT: Strong, Peter
; TITLE OF INVENTION: Recombinant Surfactant Protein D Compositions and Methods of Use
; FILE REFERENCE: 18396/2402
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; CURRENT APPLICATION NUMBER: US/10/830,959
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: PCT/GB02/04824
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: GB 0125638.7
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: GB 0209619.6
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-830-959-6

Query Match      24.8%; Score 34; DB 5; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 6; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy      10 AHLKQEIATALEQEIATALE 27
Db      3 ASLRQQLALQGLQVQLHQ 20

RESULT 26
US-10-979-683-19
; Sequence 19, Application US/10979683
; Publication No. US20050143302A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CPDV
; CURRENT APPLICATION NUMBER: US/10/979,683
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: 09/847,940
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD peptides
US-10-979-683-19

Query Match      24.8%; Score 34; DB 5; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

Qy      3 RALKWKNHLKQEIATALEQE 22
Db      11 RRMWKKTL--DASALQTE 28

RESULT 27
US-10-900-399-16
; Sequence 16, Application US/10900399
; Publication No. US20050158823A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/900,399
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
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; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-900-399-16

Query Match      24.8%; Score 34; DB 5; Length 28;
Best Local Similarity 39.1%; Pred. No. 1.9e+03;
Matches 9; Conservative 6; Mismatches 4; Indels 4; Gaps 1;

QY      10 AHLKQEIQAIEQEI-----AALEQ 28
        ||::||::||::||::||
Db       3 ASLRQQLALQGQLHQAALSQ 25

RESULT 28
US-11-032-630-32
; Sequence 32, Application US/11032630
; Publication No. US20050208036A1
; GENERAL INFORMATION:
; APPLICANT: Blazer, Bruce R
; APPLICANT: O'Shaughnessy, Mathew J
; APPLICANT: Vogtenhuber, Christine
; APPLICANT: Serody, Jonathan S
; APPLICANT: Albert, Baldwin S
; TITLE OF INVENTION: METHODS FOR TREATING OR PREVENTING GVHD
; FILE REFERENCE: 421/115/2
; CURRENT APPLICATION NUMBER: US/11/032,630
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/374,222
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant non-functional MTD-NBD fusion polypeptide
US-11-032-630-32

Query Match      24.8%; Score 34; DB 6; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY      3 RALKWKNAHLKQEIQAIEAQE 22
        ||::||::||::||::||
Db      11 RRWKWKKTAL--DASALQTE 28

RESULT 29
US-09-864-761-42292
; Sequence 42292, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42292
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008392.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
US-09-864-761-42292

Query Match      24.5%; Score 33.5; DB 3; Length 28;
Best Local Similarity 34.6%; Pred. No. 2.2e+03;
Matches 9; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY      3 RALKWKNAHLKQEIQAIEQAIEAQE 28
        ||::||::||::||::||
Db       3 RLLKGR-AQVQAEIEELQEQTRALDK 27

RESULT 30
US-10-267-682-85
; Sequence 85, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
```

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Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-682-85
Query Match 24.1%; Score 33; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 2.5e+03;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 5 LKWNHKLKORIALAEQIEIAL 26
| : | : | : | : | : |
Db 4 LQAEVDLEDEKSALEQTEIAL 25

RESULT 31
US-10-267-748-85
Sequence 85, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-748-85
Query Match 24.1%; Score 33; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 2.5e+03;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 5 LKWNHKLKORIALAEQIEIAL 26
| : | : | : | : | : |
Db 4 LQAEVDLEDEKSALEQTEIAL 25

RESULT 32
US-10-023-066A-58
Sequence 58, Application US/10023066A
Publication No. US20030056242A1
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE AND
THREONINE CONTENT OF THE SEEDS OF
PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
```

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/
/
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 58:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-023-066A-58

Query Match      23.4%; Score 32; DB 4; Length 28;
Best Local Similarity 20.0%; Pred. No. 3.4e+03;
Matches 5; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETAALEQETAA 25
   |::||:|::|::|::|::|
Db 4 KMKAMEEKLKMKMEELKMKMEKMA 28

RESULT 33
US-10-652-244-17
/ Sequence 17, Application US/10652244
/ Publication No. US20040052788A1
/ GENERAL INFORMATION:
/ APPLICANT: Wiley, Raymond R.
/ TITLE OF INVENTION: Cytokine that Induces Apoptosis
/ FILE REFERENCE: 2835-E
/ CURRENT APPLICATION NUMBER: US/10/652,244
/ PRIOR FILING DATE: 2003-09-02
/ PRIOR APPLICATION NUMBER: US/09/796,581
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: 09/320,424
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: 09/190,046
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: 09/048,641
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 08/670,354
/ PRIOR FILING DATE: 1996-06-25
/ PRIOR APPLICATION NUMBER: 08/548,368
/ PRIOR FILING DATE: 1995-11-01
/ PRIOR APPLICATION NUMBER: 08/496,632
/ PRIOR FILING DATE: 1995-06-29
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: LZ peptide
US-10-652-244-17

Query Match      23.4%; Score 32; DB 4; Length 28;
Best Local Similarity 34.8%; Pred. No. 3.4e+03;
Matches 8; Conservative 7; Mismatches 4; Indels 1;

QY 10 AHLKQETAALEQETI---AALEQ 28
   |::||:|::|::|::|
Db 3 ASIRQETAEIQGQIQHQAISQ 25

RESULT 34
US-10-804-678-58
/ Sequence 58, Application US/10804678
/ Publication No. US20050005330A1
```

```
/
/
/ GENERAL INFORMATION:
/ APPLICANT: EPELBAUM, SABINE URSULA
/ FALCO, SAVERIO CARL
/ MCDEVITT, RAYMOND ERVIN, III
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE CONTENT OF
/ THE SEEDS OF PLANTS
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: E. I. DU PONT DE NEMOURS AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.50 INCH
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: MICROSOFT OFFICE 97
/ SOFTWARE: MICROSOFT WINDOWS 95
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/804,678
/ FILING DATE: 19-Mar-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/049,304
/ FILING DATE: 27-Mar-1998
/ APPLICATION NUMBER: 08/824,627
/ FILING DATE: MARCH 27, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CHRISTENBURY, LYNNE M.
/ REGISTRATION NUMBER: 30,971
/ REFERENCE/DOCKET NUMBER: BB-1037-F
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-5481
/ TELEFAX: 302-892-7949
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 58:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-804-678-58

Query Match      23.4%; Score 32; DB 5; Length 28;
Best Local Similarity 20.0%; Pred. No. 3.4e+03;
Matches 5; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETAALEQETAA 25
   |::||:|::|::|::|
Db 4 KMKAMEEKLKMKMEELKMKMEKMA 28

RESULT 35
US-10-900-399-17
/ Sequence 17, Application US/10900399
/ Publication No. US20050158823A1
/ GENERAL INFORMATION:
/ APPLICANT: Wiley, Steven R.
/ APPLICANT: Goodwin, Raymond G.
/ TITLE OF INVENTION: Cytokine that Induces Apoptosis
/ FILE REFERENCE: 2835-E
/ CURRENT APPLICATION NUMBER: US/10/900,399
/ CURRENT FILING DATE: 2004-07-28
/ PRIOR APPLICATION NUMBER: US/09/796,581
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: 09/320,424
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: 09/190,046
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: 09/048,641
```


Tue Nov 22 08:14:37 2005

;
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-900-399-17

Query Match 23.4%; Score 32; DB 5; Length 28;
Best Local Similarity 34.8%; Pred. No. 3.4e+03;
Matches 8; Conservative 7; Mismatches 4; Indels 4; Gaps 1;

Qy 10 AHLKQETIAALEQEI-----ALEQ 28
Db 3 ASIRQQIEATGGQIQHQAISQ 25

RESULT 36
US-09-864-761-43156
; Sequence 43156, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

;
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43156
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: MAP TO AL049565.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 0.94
; OTHER INFORMATION: EST_HUMAN HIT: AW821909.1, EVALUO 2.70e-02
US-09-864-761-43156

Query Match 22.6%; Score 31; DB 3; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LKWKNAHLKQEI 16
Db 14 LQWNNGFLKIEL 25

RESULT 37
US-10-252-136-16
; Sequence 16, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-16

Query Match 22.6%; Score 31; DB 4; Length 28;
Best Local Similarity 29.4%; Pred. No. 4.6e+03;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 WKNAHLKQETIAALEQEI 23
Db 8 WKDLKSLLEVKDEL 24

RESULT 38
US-10-351-641-494
; Sequence 494, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

Query Match 22.6%; Score 31; DB 4; Length 28;
Best Local Similarity 29.4%; Pred. No. 4.6e+03;

Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 WKNAHLKQEIATLAEQEI 23
||: ||: ||: ||:
Db 8 WKDLKSLLEVKDEL 24

RESULT 41

US-09-746-742-25
; Sequence 25, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Soluble, Trimeric Version of the Coiled Coil
; OTHER INFORMATION: Region to GCN4 in IQN17
US-09-746-742-25

Query Match 21.9%; Score 30; DB 3; Length 28;
Best Local Similarity 28.6%; Pred. No. 6.3e+03;
Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIATLAEQ 21
||: ||: ||: ||:
Db 8 KIEETESKQKKIENIARIKK 28

RESULT 42

US-10-080-608A-2
; Sequence 2, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Unknown

; FEATURE:
; OTHER INFORMATION: Probable variant of hómo sapiens protein.
US-10-080-608A-2

Query Match 21.9%; Score 30; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 6.3e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 5 LKWKNAHLKQEIATLAEQEI 26
||: ||: ||: ||:
Db 4 LQAEITDQLEDEKVALQTEIANL 25

RESULT 43

US-10-370-685-91
; Sequence 91, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF-P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 28
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: leucine zipper sequence
US-10-370-685-91

Query Match 21.9%; Score 30; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 6.3e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 5 LKWKNAHLKQEIATLAEQEI 26
||: ||: ||: ||:
Db 4 LQAEITDQLEDEKVALQTEIANL 25

RESULT 44

US-10-267-682-86
; Sequence 86, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 86:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-267-748-86

Query Match          21.9%; Score 30; DB 4; Length 28;
Best Local Similarity 27.3%; Pred. No. 6.3e+03;
Matches      6; Conservative    6; Mismatches   10; Indels     0; Gaps      0;

QY       1 KIRALKWKNAHLKQEIAALEQE 22
         |::|||::|::|
DB        7 KVTKLKAQNSELASTANMLREQ 28

Search completed: November 21, 2005, 22:04:03
Job time : 106.5 secs
```

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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:46:35 ; Search time 4 Seconds
(without alignments)
7.909 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWNAHLKQETAALEQIAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 45

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	17.5	28	7	US-11-019-894A-21
2	20	14.6	28	1	US-10-983-464-22
3	18	13.1	28	1	US-10-939-890-355
4	18	13.1	28	1	US-10-939-890-831
5	16	11.7	28	1	US-10-632-349-4
6	16	11.7	28	1	US-10-939-890-345
7	16	11.7	28	1	US-10-938-890-351
8	16	11.7	28	1	US-10-939-890-382
9	16	11.7	28	1	US-10-939-890-698
10	16	11.7	28	1	US-10-939-890-821
11	16	11.7	28	1	US-10-939-890-827
12	16	11.7	28	1	US-10-997-201A-13
13	15	10.9	28	1	US-10-938-890-353
14	15	10.9	28	1	US-10-939-890-384
15	15	10.9	28	1	US-10-939-890-829
16	15	10.9	28	7	US-11-096-706-213
17	14	10.2	28	1	US-10-939-890-325
18	14	10.2	28	1	US-10-939-890-326
19	14	10.2	28	1	US-10-939-890-344
20	14	10.2	28	1	US-10-939-890-356
21	14	10.2	28	1	US-10-939-890-630
22	14	10.2	28	1	US-10-939-890-719
23	14	10.2	28	1	US-10-939-890-721
24	14	10.2	28	1	US-10-939-890-722
25	14	10.2	28	1	US-10-939-890-794

26	14	10.2	28	1	US-10-939-890-795
27	14	10.2	28	1	US-10-939-890-820
28	14	10.2	28	1	US-10-939-890-832
29	14	10.2	28	1	US-10-939-890-847
30	14	10.2	28	7	US-11-021-441-50
31	13	9.5	28	1	US-10-939-890-346
32	13	9.5	28	1	US-10-939-890-383
33	13	9.5	28	1	US-10-939-890-699
34	13	9.5	28	1	US-10-939-890-822
35	13	9.5	28	7	US-11-109-161-3
36	12	8.8	28	1	US-10-986-501-294
37	12	8.8	28	1	US-10-939-890-385
38	12	8.8	28	1	US-10-939-890-464
39	12	8.8	28	1	US-10-939-890-701
40	12	8.8	28	1	US-10-939-890-720
41	12	8.8	28	1	US-10-939-890-723
42	12	8.8	28	7	US-11-022-562-236
43	11	8.0	28	1	US-10-716-189-10
44	11	8.0	28	1	US-10-939-890-474
45	11	8.0	28	1	US-10-939-890-726

ALIGNMENTS

RESULT 1
US-11-019-894A-21
; Sequence 21, Application US/11019894A
; Publication No. US20050245451A1
; GENERAL INFORMATION:
; APPLICANT: Pincus, Matthew R.
; TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED
; TITLE OF INVENTION: MAMMALIAN CELLS
; FILE REFERENCE: 1181-17 CIP A
; CURRENT APPLICATION NUMBER: US/11/019,894A
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: 10/386,737
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/827,683
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,102
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/363,785
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide; Human C-JUN membrane penetrating leader sequence
US-11-019-894A-21

Query Match 17.5%; Score 24; DB 7; Length 28;
Best Local Similarity 25.0%; Pred. No. 1e+02;
Matches 6; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
QY 5 LKWNNAHLKQETAALEQIAALEQ 28
Db 2 IKAERKMRNRITAAASKSRKRLER 25

RESULT 2
US-10-983-464-22
; Sequence 22, Application US/10983464
; Publication No. US20050245446A1
; GENERAL INFORMATION:
; APPLICANT: Hailes, Helen C.
; APPLICANT: Tabor, John B.
; APPLICANT: Wong, John B.
; APPLICANT: Pilkington-Miksa, Michael
; APPLICANT: Hart, Stephen L.

```
; APPLICANT: Hurley, Christopher A.
; TITLE OF INVENTION: Materials For The Delivery of
; FILE OF INVENTION: Biologically-Active Material To Cells
; FILE REFERENCE: 50318/008001
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: US/10/983,464
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: PCT/GB03/01985
; PRIOR FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: US 60/576,270
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-983-464-22

Query Match      14.6%; Score 20; DB 1; Length 28;
Best Local Similarity 29.2%; Pred. No. 4e+02;
Matches 7; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY      1 KIRALKWNAHLKQETAAALEQETA 24
        | : | : | : | : | : | : |
Db      1 KKKKKKKKKKKKKKKKKKKGACRRETA 24

RESULT 3
US-10-939-890-355
; Sequence 355, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (16)..(16)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)..(21)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
```

```
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-355

Query Match      13.1%; Score 18; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 KNAHLK 13
        | : | : |
Db      16 KTAYMK 21

RESULT 4
US-10-939-890-831
; Sequence 831, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 831
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (16)..(16)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)..(21)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
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Tue Nov 22 08:14:37 2005

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; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-831

Query Match      13.1%; Score 18; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      8 KNAHLK 13
Db      16 KTAYMK 21

RESULT 5
US-10-632-349-4
; Sequence 4, Application US/10632349
; Publication No. US20050250685A1
; GENERAL INFORMATION:
; APPLICANT: ZAVERI, CHANDA
; TITLE OF INVENTION: PEPTIDES WITH WOUND HEALING ACTIVITY
; FILE REFERENCE: 37896.00002.DIV3
; CURRENT APPLICATION NUMBER: US/10/632.349
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 09/879,666
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/211,859
; PRIOR FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Acetylation
US-10-632-349-4

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      12 LKQBIALAEQ 21
Db      16 LKEKKEVVEE 25

RESULT 6
US-10-939-890-345
; Sequence 345, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351

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; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 345
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-345

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      7 WKNAHLK 13
Db      7 WTPHPHK 13

RESULT 7
US-10-939-890-351
; Sequence 351, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351

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; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-351

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 23.1%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      7 WKNAHLKQETAAAL 19
Db      10 WEQVVLHDDAQVL 22

RESULT 8
US-10-939-890-382
; Sequence 382, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JU spacer linker
US-10-939-890-698

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KW 7
Db      10 KW 11

RESULT 10
US-10-939-890-821
; Sequence 821, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
```



```

; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a iv-dde linker
US-10-939-890-821

Query Match 11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 WKNAHLK 13
Db 7 WTPHPK 13

RESULT 11
US-10-939-890-827
; Sequence 827, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong

; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-827

Query Match 11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 23.1%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 7 WKNAHLKQETAAAL 19
Db 10 WEQVVLHDDAQVL 22

RESULT 12
US-10-997-201A-13
; Sequence 13, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-13
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Query Match 11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 5; Indels

Qy	10	AHLKQEIAALEQ	21
		: : :	
Dp	6	AYKODEKVASDO	17

RESULT 13

US-10-939-890-353
; Sequence 353, Application US/10939890
: Publication No. US20050250700A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 384
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
/ US-10-939-890-384

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Query Match 10.9%; Score 15; bB 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 2e+03;
Matches 3: Conservative 2; Mismatches 5; Indels

QY 6 KWKNAHLKQE 15
: | : | : |
Db 2 OWYHDGLHNE 11

RESULT 15

US-10-939-890-829
; Sequence 829, Application US/10939890
; Publication No. US20050250700A1

FEATURE: ;
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-353

Query Match	10.9%	Score 15;	DB 1;	Length 28;
Best Local Similarity	66.7%;	Pred. No. 2e+03;		
Matches	2;	Conservative	0;	Mismatches 1;
Indels	0;	Gaps	0;	

QY 7 WKN 9
11 W.N 13

RESULT 14

US-10-939-890-384
; Sequence 384, Application US/10939890
; Publication No. US20050250700A1

APPLICANT: Sato, Aaron K.

APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 829
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLTATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-829
Query Match 10.9%; Score 15; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 WKN 9
Db 11 WLN 13
RESULT 16
US-11-096-706-213
Sequence 213, Application US/11096706
Publication No. US20050245476A1
GENERAL INFORMATION:
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
FILE REFERENCE: 019496-008220US
CURRENT APPLICATION NUMBER: US/11/096,706
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 60/560,535
PRIOR FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US 60/576,757
PRIOR FILING DATE: 2004-06-02
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn version 3.3
SEQ ID NO 213
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Chemically synthesized peptide (DNA binding domain)
US-11-096-706-213
Query Match 10.9%; Score 15; DB 7; Length 28;
Best Local Similarity 33.3%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 8 KNAHLKQEI 16

Db 12 RSDHLATTHI 20
RESULT 17
US-10-939-890-325
Sequence 325, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 325
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-325
Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 2.6e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 7 WKN 9
Db 12 WRS 14
RESULT 18
US-10-939-890-326
Sequence 326, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong

```
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 326
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-326

Query Match          10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 QEI 16
      |||
Db      10 QEI 12

RESULT 19
US-10-939-890-344
/ Sequence 344, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 326
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-326
```

```
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 344
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-344

Query Match          10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 ALKW 7
      | : |
Db      7 AQQM 10

RESULT 20
US-10-939-890-356
/ Sequence 356, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 356
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-356

Query Match      10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      15 EIAALEQEI 23
      || : :
Db      8 EILSMADQL 16

RESULT 21
US-10-939-890-630
; Sequence 630, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-630

Query Match      10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      15 EIAALEQEI 23
      || : :
Db      8 EILSMADQL 16

US-10-939-890-719
; Sequence 719, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 719
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-719

Query Match      10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      15 EIAALEQEI 23
      || : :
Db      8 EILSMADQL 16

US-10-939-890-721
; Sequence 721, Application US/10939890
```

```

; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 721
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
US-10-939-890-721

```

```

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Caps 0;

```

```

QY 15 EIAALEQEI 23
DB 8 EILSMADQL 16

```

```

RESULT 24
US-10-939-890-722
; Sequence 722, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe

```

```

; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 722
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-722

```

```

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Caps 0;

```

```

QY 15 EIAALEQEI 23
DB 8 EILSMADQL 16

```

```

RESULT 25
US-10-939-890-794
; Sequence 794, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle

```

RESULT 26
US-10-939-890-795
; Sequence 795, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronoski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939.890

RESULT 27

US-10-939-890-820

Sequence 820, Application US/10939890

Publication No. US20050250700A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Sexton, Daniel J.

APPLICANT: Dransfield, Daniel T.

APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe

APPLICANT: Bussat, Philippe

APPLICANT: Fan, Hong

APPLICANT: Khurana, Sudha

APPLICANT: Linder, Karen E.

APPLICANT: Marinelli, Edmund R.

APPLICANT: Nanjappan, Palaniappa

APPLICANT: Nunn, Adrian D.

APPLICANT: Pillai, Radhakrishna

APPLICANT: Pocheon, Sibylle

APPLICANT: Ramalingam, Kondareddiar

APPLICANT: Shrivastava, Ajay

APPLICANT: Song, Bo

APPLICANT: Swenson, Rolf E.

APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

FILE REFERENCE: D0617.70014US00

CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

```
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 820
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(4)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-820
```

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
QY 4 ALKW 7
Db | : |
7 AQQW 10
```

RESULT 28

```
US-10-939-890-832
; Sequence 832, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617, 70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 832
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-832
```

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```
QY 15 EIAALEQEI 23
Db || : :
8 EILSMADQL 16
```

RESULT 29

```
US-10-939-890-847
; Sequence 847, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617, 70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 847
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
```


NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLTATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a J spacer linker
US-10-939-890-847

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 15 EIAALEQEI 23
|| : :
Db 8 EILSMADQL 16

RESULT 30
US-11-021-441-50
Sequence 50, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: PORTNOY, Daniel A., Jr.
APPLICANT: LUKEFT, William S., Jr.
APPLICANT: COOK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021.441
CURRENT FILING DATE: 2004-12-23
PRIOR FILING DATE: 2004-10-06
PRIOR FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US 10/883,599
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 28
TYPE: PRT
ORGANISM: Bacillus anthracis
US-11-021-441-50

Query Match 10.2%; Score 14; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 LKQETIAAL 19
|| : :
Db 4 LKQASCAL 11

RESULT 31
US-10-939-890-346
Sequence 346, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe

APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 893
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 346
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-346

Query Match 9.5%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ALE 20
|| : :
Db 4 ALE 6

RESULT 32
US-10-939-890-383
Sequence 383, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 383
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-939-890-383

Query Match 9.5%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ALE 20
Db |||
4 ALE 6

RESULT 33
US-10-939-890-699
; Sequence 699, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 28
; TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
; US-10-939-890-699

Query Match 9.5%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ALE 20
Db |||
4 ALE 6

RESULT 34
US-10-939-890-822
; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 822
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:

```
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (26)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JV spacer linker
US-10-939-890-822

Query Match
Best Local Similarity 9.5%; Score 13; DB 1; Length 28;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ALE 20
Db 4 ALE 6

RESULT 35
US-11-109-161-3
; Sequence 3, Application US/11109161
; Publication No. US20050244422A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, Desmond
; APPLICANT: SINGH, Baljit K.
; TITLE OF INVENTION: METHODS FOR DELIVERING MED
; TITLE OF INVENTION: PEPTIDE-LINKED AGENT INTO CELLS UNDER CONDITIONS OF CELLULAR
; TITLE OF INVENTION: STRESS
; FILE REFERENCE: 51490-20003.00
; CURRENT APPLICATION NUMBER: US/11/109,161
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/563,141
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/563,676
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/657,826
; PRIOR FILING DATE: 2005-03-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-109-161-3

Query Match
Best Local Similarity 9.5%; Score 13; DB 7; Length 28;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RALKW 7
Db 18 RGFCW 22

RESULT 36
US-10-986-501-294
; Sequence 294, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
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; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-294

Query Match
Best Local Similarity 8.8%; Score 12; DB 1; Length 28;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HL 12
Db 15 HL 16

RESULT 37
US-10-939-890-385
; Sequence 385, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 385
; LENGTH: 28
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-385

Query Match 8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ALKW 7
| |
Db 1 AQDW 4

RESULT 38

US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-701

Query Match 8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ALKW 7
| |
Db 1 AQDW 4

RESULT 40

US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.

Qy 6 KW 7
: |
Db 2 EW 3

RESULT 39

```

; APPLICANT: Arbogast, Christophe
; APPLICANT: Buesat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-01-15
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 720
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720

Query Match      8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 KW 7
Db      2 EW 3

RESULT 41
US-10-939-890-723
; Sequence 723, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Buesat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.

Query Match      8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 KW 7
Db      2 EW 3

RESULT 42
US-11-022-562-236
; Sequence 236, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-236

Query Match      8.8%; Score 12; DB 7; Length 28;

```

Best Local Similarity 50.0%; Pred. No. 4.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 2;

QY 17 AALE 20
|:::
Db 24 AAMQ 27

RESULT 43

US-10-716-189-10
; Sequence 10, Application US/10716189
; Publication No. US20050249750A1
; GENERAL INFORMATION:
; APPLICANT: Nardin, Elizabeth
; APPLICANT: Moreno, Alberto
; TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
; FILE REFERENCE: 5986/1B615-US1
; CURRENT APPLICATION NUMBER: US/10/716,189
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/060,450
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: 60/033,916
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of Carboxyl Terminus of SEQ ID NO:4 to
; OTHER INFORMATION: Amino Terminus of Seq ID NO: 1, designated T1B
US-10-716-189-10

Query Match 8.0%; Score 11; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 NAH 11
|:::
Db 1 NAN 3

RESULT 44

US-10-939-890-474
; Sequence 474, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-474

Query Match 8.0%; Score 11; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 W 7
| W 1
Db 1 W 1

RESULT 45

US-10-939-890-726
; Sequence 726, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 726
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide

```

; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-726

```

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Query Match      8.0%; Score 11; DB 1; Length 28;
Best Local Similarity 100.0%; Pred.No. 5e+03;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      7 W 7
Db      1 W 1

```

Search completed: November 21, 2005, 22:04:16
Job time : 4.5 secs

